

Seq. ID LIB3150-047-Q1-N1-F4
Method BLASTX
NCBI GI g3122386
BLAST score 254
E value 4.0e-22
Match length 62
% identity 79
NCBI Description WD-40 REPEAT PROTEIN MSI1 >gi_2394227 (AF016845) WD-40 repeat protein [Lycopersicon esculentum]

Seq. No. 297816
Seq. ID LIB3150-047-Q1-N1-H7
Method BLASTX
NCBI GI 94586111
BLAST score 194
E value 8.0e-15
Match length 82
% identity 57
NCBI Description (AL049638) putative protein [Arabidopsis thaliana]

Seq. No. 297817
Seq. ID LIB3150-048-Q1-N1-B10
Method BLASTX
NCBI GI g2245136
BLAST score 154
E value 9.0e-11
Match length 64
% identity 44
NCBI Description (Z97344) trehalose-6-phosphate synthase homolog
[Arabidopsis thaliana]

Seq. No. 297818
Seq. ID LIB3150-048-Q1-N1-C7
Method BLASTX
NCBI GI 91184776
BLAST score 271
E value 3.0e-24
Match length 67
% identity 82
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
GAPC4 [Zea mays]

Seq. No. 297819
Seq. ID LIB3150-048-Q1-N1-C9
Method BLASTX
NCBI GI 91184774
BLAST score 248
E value 6.0e-32
Match length 78
% identity 95
NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
GAPC3 [Zea mays]

Seq. No. 297820
Seq. ID LIB3150-048-Q1-N1-D1
Method BLASTN
NCBI GI q168606

BLAST score 53
E value 3.0e-21
Match length 104
% identity 88
NCBI Description Zea mays mitochondrial Rieske Fe-S protein mRNA, complete cds

Seq. No. 297821
Seq. ID LIB3150-048-Q1-N1-F2
Method BLASTX
NCBI GI g4104060
BLAST score 316
E value 3.0e-29
Match length 112
% identity 55
NCBI Description (AF031231) S222 [Triticum aestivum]

Seq. No. 297822
Seq. ID LIB3150-048-Q1-N1-H10
Method BLASTN
NCBI GI g168419
BLAST score 64
E value 1.0e-27
Match length 108
% identity 90
NCBI Description Maize (Z.mays) aldolase mRNA, complete cds

Seq. No. 297823
Seq. ID LIB3150-048-Q1-N1-H5
Method BLASTX
NCBI GI g1076800
BLAST score 317
E value 3.0e-29
Match length 68
% identity 90
NCBI Description L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme - maize >gi_600116_emb_CAA84406 (Z34934) cytosolic ascorbate peroxidase [Zea mays] >gi_1096503_prf_2111423A ascorbate peroxidase [Zea mays]

Seq. No. 297824
Seq. ID LIB3150-049-Q1-N1-A3
Method BLASTX
NCBI GI g2944417
BLAST score 318
E value 2.0e-29
Match length 98
% identity 64
NCBI Description (AF049881) peroxidase FLXPER4 [Linum usitatissimum]

Seq. No. 297825
Seq. ID LIB3150-049-Q1-N1-A5
Method BLASTX
NCBI GI g1184776
BLAST score 377
E value 3.0e-36
Match length 107

% identity 75
 NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
 GACP4 [Zea mays]

Seq. No. 297826
 Seq. ID LIB3150-049-Q1-N1-C7
 Method BLASTX
 NCBI GI g2286151
 BLAST score 326
 E value 2.0e-30
 Match length 111
 % identity 64
 NCBI Description (AF007580) translation initiation factor [Zea mays]

Seq. No. 297827
 Seq. ID LIB3150-049-Q1-N1-C9
 Method BLASTX
 NCBI GI g1345587
 BLAST score 324
 E value 4.0e-32
 Match length 97
 % identity 79
 NCBI Description 14-3-3-LIKE PROTEIN GF14-6 >gi_998430_bbs_164522 (S77133)
 GF14-6=14-3-3 protein homolog [Zea mays, XL80, Peptide, 261
 aa] [Zea mays]

Seq. No. 297828
 Seq. ID LIB3150-049-Q1-N1-D4
 Method BLASTX
 NCBI GI g118104
 BLAST score 479
 E value 3.0e-48
 Match length 123
 % identity 76
 NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
 (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) -
 >gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
 maize >gi_168461 (M55021) cyclophilin [Zea mays]
 >gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 297829
 Seq. ID LIB3150-049-Q1-N1-E1
 Method BLASTX
 NCBI GI g2464864
 BLAST score 242
 E value 1.0e-20
 Match length 96
 % identity 47
 NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 297830
 Seq. ID LIB3150-049-Q1-N1-E12
 Method BLASTX
 NCBI GI g4539006
 BLAST score 424
 E value 7.0e-42
 Match length 123

% identity 67
NCBI Description (AL049481) putative protein [Arabidopsis thaliana]

Seq. No. 297831
Seq. ID LIB3150-049-Q1-N1-E7
Method BLASTX
NCBI GI g135411
BLAST score 514
E value 2.0e-52
Match length 109
% identity 90
NCBI Description TUBULIN ALPHA-2 CHAIN >gi_82732_pir_S15772 tubulin alpha-2 chain - maize >gi_22148_emb_CAA33733_ (X15704) alpha2-tubulin [Zea mays]

Seq. No. 297832
Seq. ID LIB3150-049-Q1-N1-F11
Method BLASTX
NCBI GI g4193320
BLAST score 405
E value 1.0e-39
Match length 119
% identity 67
NCBI Description (AF045473) histone deacetylase [Zea mays]

Seq. No. 297833
Seq. ID LIB3150-049-Q1-N1-F9
Method BLASTX
NCBI GI g134598
BLAST score 471
E value 2.0e-47
Match length 98
% identity 100
NCBI Description SUPEROXIDE DISMUTASE-4AP (CU-ZN)

Seq. No. 297834
Seq. ID LIB3150-049-Q1-N1-G4
Method BLASTX
NCBI GI g4039155
BLAST score 162
E value 4.0e-11
Match length 110
% identity 44
NCBI Description (AF104258) putative copper-inducible 35.6 kDa protein [Festuca rubra]

Seq. No. 297835
Seq. ID LIB3150-049-Q1-N1-G5
Method BLASTX
NCBI GI g112994
BLAST score 262
E value 8.0e-23
Match length 82
% identity 71
NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN >gi_82685_pir_S04536 embryonic abundant protein, glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)

ABA-inducible gene protein [Zea mays]
>gi_226091_prf_1410284A abscisic acid inducible gene [Zea mays]

Seq. No. 297836
Seq. ID LIB3150-050-Q1-N1-B9
Method BLASTX
NCBI GI g3242789
BLAST score 472
E value 2.0e-47
Match length 130
% identity 62
NCBI Description (AF055357) respiratory burst oxidase protein D [Arabidopsis thaliana]

Seq. No. 297837
Seq. ID LIB3150-050-Q1-N1-C11
Method BLASTX
NCBI GI g1709619
BLAST score 259
E value 1.0e-22
Match length 99
% identity 56
NCBI Description PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) / DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE (GLYCOSYLATION SITE-BINDING CHAIN) (GSBP)
>gi_2146814_pir_S69181 protein disulfide isomerase (EC 5.3.4.1) precursor - maize >gi_625148 (L39014) protein disulfide isomerase [Zea mays]

Seq. No. 297838
Seq. ID LIB3150-050-Q1-N1-D11
Method BLASTX
NCBI GI g1321661
BLAST score 265
E value 2.0e-23
Match length 60
% identity 85
NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]

Seq. No. 297839
Seq. ID LIB3150-050-Q1-N1-D8
Method BLASTX
NCBI GI g1350986
BLAST score 202
E value 5.0e-16
Match length 69
% identity 64
NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
>gi_483431_dbj_BAA05059_ (D26060) cyc07 [Oryza sativa]

Seq. No. 297840
Seq. ID LIB3150-050-Q1-N1-D9
Method BLASTX
NCBI GI g629861
BLAST score 209
E value 3.0e-21

Match length 76
% identity 80
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 297841
Seq. ID LIB3150-050-Q1-N1-E6
Method BLASTX
NCBI GI g4585900
BLAST score 228
E value 7.0e-19
Match length 76
% identity 68
NCBI Description (AC007133) putative histone H2A [Arabidopsis thaliana]

Seq. No. 297842
Seq. ID LIB3150-050-Q1-N1-F1
Method BLASTN
NCBI GI g3015620
BLAST score 39
E value 1.0e-12
Match length 63
% identity 90
NCBI Description Zea mays low molecular weight heat shock protein precursor
(hsp22) mRNA, nuclear gene encoding mitochondrial protein,
complete cds

Seq. No. 297843
Seq. ID LIB3150-050-Q1-N1-F7
Method BLASTX
NCBI GI g4455283
BLAST score 178
E value 1.0e-17
Match length 97
% identity 55
NCBI Description (AL035527) L1 specific homeobox gene ATML1/ovule-specific
homeobox protein A20 [Arabidopsis thaliana]

Seq. No. 297844
Seq. ID LIB3150-050-Q1-N1-G10
Method BLASTX
NCBI GI g1658313
BLAST score 206
E value 2.0e-23
Match length 85
% identity 34
NCBI Description (Y08987) osr40g2 [Oryza sativa]

Seq. No. 297845
Seq. ID LIB3150-050-Q1-N1-G11
Method BLASTN
NCBI GI g260552
BLAST score 34
E value 1.0e-09
Match length 38
% identity 97
NCBI Description Wx (wx-B2) {transposable element Tourist-Zml} [Zea

mays=corn, Transposon Mutant, 150 nt]

Seq. No. 297846
Seq. ID LIB3150-050-Q1-N1-H11
Method BLASTX
NCBI GI g1885348
BLAST score 159
E value 3.0e-11
Match length 47
% identity 77
NCBI Description (X91515) histone H4 [Trichogramma caceociae]

Seq. No. 297847
Seq. ID LIB3150-050-Q1-N1-H9
Method BLASTX
NCBI GI g1346251
BLAST score 208
E value 2.0e-16
Match length 53
% identity 79
NCBI Description HISTONE H2B.4 >gi_577819_emb_CAA49585_ (X69961) H2B histone [Zea mays]

Seq. No. 297848
Seq. ID LIB3150-051-Q1-N1-B9
Method BLASTX
NCBI GI g1709000
BLAST score 422
E value 1.0e-41
Match length 88
% identity 92
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_960357_dbj_BAA09895_ (D63835) S-adenosylmethionine synthetase [Hordeum vulgare]

Seq. No. 297849
Seq. ID LIB3150-051-Q1-N1-C10
Method BLASTX
NCBI GI g133961
BLAST score 260
E value 1.0e-22
Match length 68
% identity 78
NCBI Description 40S RIBOSOMAL PROTEIN S4 (OMNIPOTENT SUPPRESSOR PROTEIN SUP44) (RP12) (S2E) >gi_70888_pir_R3BYS2 ribosomal protein S2.e - yeast (Saccharomyces cerevisiae) >gi_172793 (M59375) ribosomal protein S4 [Saccharomyces cerevisiae] >gi_1322683_emb_CAA96831_ (Z72645) ORF YGL123w [Saccharomyces cerevisiae] >gi_1628451_emb_CAA63835_ (X94106) SUP44 [Saccharomyces cerevisiae]

Seq. No. 297850
Seq. ID LIB3150-051-Q1-N1-C7
Method BLASTX
NCBI GI g3334756
BLAST score 224

0963401
* 10000

E value 2.0e-18
Match length 88
% identity 57
NCBI Description (Y16672) putative arginine/serine-rich splicing factor
[Medicago sativa]

Seq. No. 297851
Seq. ID LIB3150-051-Q1-N1-D5
Method BLASTX
NCBI GI g730536
BLAST score 529
E value 2.0e-54
Match length 103
% identity 97
NCBI Description 60S RIBOSOMAL PROTEIN L23 >gi_310933 (L18915) 60S ribosomal
protein subunit L17 [Nicotiana tabacum]

Seq. No. 297852
Seq. ID LIB3150-051-Q1-N1-G3
Method BLASTX
NCBI GI g1184776
BLAST score 598
E value 3.0e-62
Match length 114
% identity 100
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
GAPC4 [Zea mays]

Seq. No. 297853
Seq. ID LIB3150-051-Q1-N1-H6
Method BLASTX
NCBI GI g2293566
BLAST score 185
E value 2.0e-16
Match length 53
% identity 96
NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]

Seq. No. 297854
Seq. ID LIB3150-052-Q1-N1-B2
Method BLASTX
NCBI GI g122087
BLAST score 471
E value 3.0e-47
Match length 120
% identity 81
NCBI Description HISTONE H3 >gi_81849_pir_S04520 histone H3 (clone pH3c-1)
- alfalfa >gi_82609_pir_A26014 histone H3 - wheat
>gi_19607_emb_CAA31964 (X13673) histone H3 (AA 1-136)
[Medicago sativa] >gi_19609_emb_CAA31965 (X13674) histone
H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451
(X00937) H3 histone [Triticum aestivum] >gi_488565 (U09459)
histone H3.1 [Medicago sativa] >gi_2565419 (AF026803)
histone H3 [Onobrychis viciifolia]

Seq. No. 297855
Seq. ID LIB3150-052-Q1-N1-B5

Method BLASTX
NCBI GI g1184774
BLAST score 594
E value 1.0e-61
Match length 114
% identity 99
NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
GAPC3 [Zea mays]

Seq. No. 297856
Seq. ID LIB3150-052-Q1-N1-C2
Method BLASTN
NCBI GI g22144
BLAST score 171
E value 1.0e-91
Match length 218
% identity 96
NCBI Description Maize anaerobically regulated gene for fructose
bisphosphate aldolase (EC 4.1.2.13)

Seq. No. 297857
Seq. ID LIB3150-052-Q1-N1-E12
Method BLASTX
NCBI GI g131772
BLAST score 378
E value 2.0e-36
Match length 109
% identity 74
NCBI Description 40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
>gi_82723_pir_A30097 ribosomal protein S14 (clone MCH1) -
maize

Seq. No. 297858
Seq. ID LIB3150-052-Q1-N1-G11
Method BLASTX
NCBI GI g122022
BLAST score 157
E value 1.0e-10
Match length 60
% identity 60
NCBI Description HISTONE H2B >gi_283025_pir_S22323 histone H2B - wheat
>gi_21801_emb_CAA42530_ (X59873) histone H2B [Triticum
aestivum]

Seq. No. 297859
Seq. ID LIB3150-052-Q1-N1-G3
Method BLASTX
NCBI GI g133867
BLAST score 493
E value 6.0e-50
Match length 120
% identity 78
NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir_S16577 ribosomal
protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)
ribosomal protein S11 [Zea mays]

Seq. No. 297860

Seq. ID	LIB3150-053-Q1-N1-A6
Method	BLASTX
NCBI GI	g70644
BLAST score	592
E value	1.0e-61
Match length	125
% identity	18
NCBI Description	ubiquitin precursor - common sunflower (fragment)
Seq. No.	297861
Seq. ID	LIB3150-053-Q1-N1-A7
Method	BLASTX
NCBI GI	g3914402
BLAST score	247
E value	3.0e-21
Match length	97
% identity	57
NCBI Description	PROTOPORPHYRINOGEN OXIDASE, CHLOROPLAST PRECURSOR (PPO I) (PROTOPORPHYRINOGEN IX OXIDASE ISOZYME I) (PPX I) >gi_2370333_emb_CAA73865_ (Y13465) protoporphyrinogen oxidase [Nicotiana tabacum]
Seq. No.	297862
Seq. ID	LIB3150-053-Q1-N1-D10
Method	BLASTX
NCBI GI	g120670
BLAST score	495
E value	3.0e-50
Match length	121
% identity	82
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_100879_pir_S06879 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C - maize >gi_295853_emb_CAA33620_ (X15596) GAPDH [Zea mays]
Seq. No.	297863
Seq. ID	LIB3150-053-Q1-N1-D8
Method	BLASTX
NCBI GI	g266398
BLAST score	169
E value	3.0e-12
Match length	62
% identity	55
NCBI Description	TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR INHIBITOR) (CHFI) >gi_68849_pir_TIZM1 trypsin/factor XIIa inhibitor precursor - maize >gi_22327_emb_CAA37998_ (X54064) corn Hageman factor inhibitor [Zea mays]
Seq. No.	297864
Seq. ID	LIB3150-053-Q1-N1-E12
Method	BLASTX
NCBI GI	g2864625
BLAST score	522
E value	2.0e-53
Match length	112
% identity	86
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 297865
Seq. ID LIB3150-053-Q1-N1-E9
Method BLASTX
NCBI GI g70644
BLAST score 291
E value 1.0e-26
Match length 94
% identity 13
NCBI Description ubiquitin precursor - common sunflower (fragment)

Seq. No. 297866
Seq. ID LIB3150-054-Q1-N1-A10
Method BLASTX
NCBI GI g4506491
BLAST score 281
E value 4.0e-25
Match length 89
% identity 63
NCBI Description replication factor C (activator 1) 4 (37kD)
>gi_1703052_sp_P35249_AC12_HUMAN ACTIVATOR 1 37 KD SUBUNIT
(REPLICATION FACTOR C 37 KD SUBUNIT) (A1 37 KD SUBUNIT)
(RF-C 37 KD SUBUNIT) (RFC37) >gi_1498256 (M87339)
replication factor C, 37-kDa subunit [Homo sapiens]

Seq. No. 297867
Seq. ID LIB3150-054-Q1-N1-B2
Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 9.0e-11
Match length 36
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 297868
Seq. ID LIB3150-054-Q1-N1-D7
Method BLASTX
NCBI GI g1654140
BLAST score 340
E value 5.0e-32
Match length 101
% identity 57
NCBI Description (U37840) lipoxygenase [Lycopersicon esculentum]

Seq. No. 297869
Seq. ID LIB3150-054-Q1-N1-D8
Method BLASTX
NCBI GI g3548802
BLAST score 149
E value 4.0e-10
Match length 41
% identity 66
NCBI Description (AC005313) axi 1-like protein [Arabidopsis thaliana]
>gi_4335769_gb_AAD17446 (AC006284) putative axil protein
[Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No. 297870
Seq. ID LIB3150-054-Q1-N1-G11
Method BLASTX
NCBI GI g399854
BLAST score 241
E value 2.0e-20
Match length 71
% identity 73
NCBI Description HISTONE H2B.2 >gi_283042_pir_S28049 histone H2B - maize
>gi_22325_emb_CAA40565_ (X57313) H2B histone [Zea mays]

Seq. No. 297871
Seq. ID LIB3150-054-Q1-N1-G5
Method BLASTX
NCBI GI g2492504
BLAST score 156
E value 1.0e-10
Match length 108
% identity 41
NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG
>gi_1669660_emb_CAA70565_ (Y09396) protein of AAA family
[Capsicum annuum]

Seq. No. 297872
Seq. ID LIB3150-054-Q1-N1-G6
Method BLASTX
NCBI GI g3608145
BLAST score 186
E value 6.0e-14
Match length 62
% identity 63
NCBI Description (AC005314) hypothetical protein [Arabidopsis thaliana]

Seq. No. 297873
Seq. ID LIB3150-054-Q1-N1-H10
Method BLASTX
NCBI GI g4519539
BLAST score 182
E value 1.0e-13
Match length 64
% identity 56
NCBI Description (AB016256) NAD-dependent sorbitol dehydrogenase [Malus
domestica]

Seq. No. 297874
Seq. ID LIB3150-055-Q1-N1-A9
Method BLASTX
NCBI GI g2266666
BLAST score 380
E value 1.0e-36
Match length 82
% identity 83
NCBI Description (Y14202) hypothetical protein [Hordeum vulgare]

Seq. No. 297875
Seq. ID LIB3150-055-Q1-N1-D10
Method BLASTN

NCBI GI g1256711
BLAST score 74
E value 1.0e-33
Match length 224
% identity 82
NCBI Description Zea mays O-methyltransferase (OMT) gene, complete cds

Seq. No. 297876
Seq. ID LIB3150-056-Q1-N1-A3
Method BLASTN
NCBI GI g340933
BLAST score 60
E value 3.0e-25
Match length 72
% identity 96
NCBI Description Zea mays 10-kDa zein gene, complete cds

Seq. No. 297877
Seq. ID LIB3150-056-Q1-N1-B6
Method BLASTX
NCBI GI g1666173
BLAST score 430
E value 1.0e-42
Match length 92
% identity 90
NCBI Description (Y09106) transcription factor [Nicotiana plumbaginifolia]

Seq. No. 297878
 Seq. ID LIB3150-056-Q1-N1-D3
 Method BLASTX
 NCBI GI g119355
 BLAST score 495
 E value 3.0e-50
 Match length 99
 % identity 99
 NCBI Description ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
 (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
 >gi_100869_pir_S16257 phosphopyruvate hydratase (EC
 4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
 [Zea mays]

Seq. No. 297879
Seq. ID LIB3150-056-Q1-N1-D9
Method BLASTX
NCBI GI g464705
BLAST score 162
E value 3.0e-11
Match length 32
% identity 94
NCBI Description 40S RIBOSOMAL PROTEIN S13 >gi_419802_pir_S30146 ribosomal protein S13.e - maize >gi_288059_emb_CAA44311_ (X62455) cytoplasmatic ribosomal protein S13 [Zea mays]

Seq. No. 297880
Seq. ID LIB3150-057-Q1-N1-A6
Method BLASTX
NCBI GI q1632831

BLAST score 171
E value 1.0e-12
Match length 36
% identity 89
NCBI Description (Z49698) orf [Ricinus communis]

Seq. No. 297881
Seq. ID LIB3150-057-Q1-N1-B5
Method BLASTX
NCBI GI g2642648
BLAST score 289
E value 4.0e-26
Match length 67
% identity 88
NCBI Description (AF033852) cytosolic heat shock 70 protein; HSC70-3 [Spinacia oleracea] >gi_2660768 (AF034616) cytosolic heat shock 70 protein [Spinacia oleracea] >gi_2660770 (AF034617) cytosolic heat shock 70 protein [Spinacia oleracea]

Seq. No. 297882
Seq. ID LIB3150-057-Q1-N1-B6
Method BLASTX
NCBI GI g4580990
BLAST score 170
E value 2.0e-14
Match length 96
% identity 48
NCBI Description (AF120335) putative transposase [Arabidopsis thaliana]

Seq. No. 297883
Seq. ID LIB3150-057-Q1-N1-B9
Method BLASTX
NCBI GI g2911067
BLAST score 160
E value 3.0e-11
Match length 80
% identity 46
NCBI Description (AL021960) UV-damaged DNA-binding protein-like [Arabidopsis thaliana]

Seq. No. 297884
Seq. ID LIB3150-057-Q1-N1-G10
Method BLASTX
NCBI GI g4056502
BLAST score 170
E value 3.0e-12
Match length 53
% identity 62
NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]

Seq. No. 297885
Seq. ID LIB3150-057-Q1-N1-H9
Method BLASTX
NCBI GI g2340947
BLAST score 301
E value 5.0e-28
Match length 59

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% identity 100
NCBI Description (X98497) ESR1g1 [Zea mays] >gi_2340951_emb_CAA68230_ (X99968) ESR1g2 [Zea mays]

Seq. No. 297886
Seq. ID LIB3150-058-Q1-N1-A3
Method BLASTX
NCBI GI g100857
BLAST score 571
E value 5.0e-59
Match length 115
% identity 97
NCBI Description Bronze-2 protein - Maize

Seq. No. 297887
Seq. ID LIB3150-058-Q1-N1-B1
Method BLASTX
NCBI GI g118104
BLAST score 371
E value 1.0e-35
Match length 95
% identity 76
NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) - maize >gi_168461 (M55021) cyclophilin [Zea mays] >gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 297888
Seq. ID LIB3150-058-Q1-N1-B11
Method BLASTX
NCBI GI g1620753
BLAST score 156
E value 2.0e-10
Match length 63
% identity 48
NCBI Description (U72942) proteinase inhibitor [Oryza sativa] >gi_2829212_gb_AAC00503_ (AF044059) proteinase inhibitor [Oryza sativa]

Seq. No. 297889
Seq. ID LIB3150-058-Q1-N1-C10
Method BLASTX
NCBI GI g3790100
BLAST score 213
E value 3.0e-17
Match length 112
% identity 49
NCBI Description (AF095520) pyrophosphate-dependent phosphofructokinase beta subunit [Citrus X paradisi]

Seq. No. 297890
Seq. ID LIB3150-058-Q1-N1-E11
Method BLASTX
NCBI GI g1184776
BLAST score 176
E value 5.0e-20

Match length 91
% identity 65
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
GAPC4 [Zea mays]

Seq. No. 297891
Seq. ID LIB3150-058-Q1-N1-F3
Method BLASTN
NCBI GI g3851527
BLAST score 54
E value 2.0e-21
Match length 141
% identity 85
NCBI Description *Hordeum vulgare* cultivar Bomi starch branching enzyme IIb
(*sbeIIb*) gene, nuclear gene encoding plastid protein,
partial cds

Seq. No. 297892
Seq. ID LIB3150-058-Q1-N1-G6
Method BLASTX
NCBI GI g2282584
BLAST score 457
E value 7.0e-46
Match length 103
% identity 83
NCBI Description (U76259) elongation factor 1-alpha [Zea mays]

Seq. No. 297893
Seq. ID LIB3150-059-Q1-N1-A8
Method BLASTX
NCBI GI g82705
BLAST score 264
E value 3.0e-23
Match length 74
% identity 80
NCBI Description lipid body-associated major protein L3 - maize (fragment)
>gi_168513 (M17225) major protein L3 [Zea mays]

Seq. No. 297894
Seq. ID LIB3150-059-Q1-N1-B10
Method BLASTX
NCBI GI g118104
BLAST score 341
E value 4.0e-34
Match length 97
% identity 77
NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
>gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
maize >gi_168461 (M55021) cyclophilin [Zea mays]
>gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 297895
Seq. ID LIB3150-059-Q1-N1-C10
Method BLASTX
NCBI GI g1184776
BLAST score 569

DRAFT BLAST REPORT

E value	7.0e-59
Match length	108
% identity	100
NCBI Description	(U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC4 [Zea mays]
Seq. No.	297896
Seq. ID	LIB3150-059-Q1-N1-C11
Method	BLASTX
NCBI GI	g133867
BLAST score	258
E value	1.0e-22
Match length	83
% identity	64
NCBI Description	40S RIBOSOMAL PROTEIN S11 >gi_82722_pir_S16577 ribosomal protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays]
Seq. No.	297897
Seq. ID	LIB3150-059-Q1-N1-C8
Method	BLASTX
NCBI GI	g134613
BLAST score	321
E value	9.0e-30
Match length	74
% identity	84
NCBI Description	SUPEROXIDE DISMUTASE-2 (CU-ZN) >gi_82727_pir_A29077 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 2 - maize >gi_168620 (M54936) superoxide dismutase 2 [Zea mays] >gi_168622 (M15175) SOD2 protein [Zea mays]
Seq. No.	297898
Seq. ID	LIB3150-059-Q1-N1-D10
Method	BLASTX
NCBI GI	g129916
BLAST score	238
E value	3.0e-20
Match length	60
% identity	80
NCBI Description	PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir_TVWTGY phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase (AA 1 - 401) [Triticum aestivum]
Seq. No.	297899
Seq. ID	LIB3150-059-Q1-N1-D11
Method	BLASTX
NCBI GI	g3334138
BLAST score	269
E value	5.0e-28
Match length	94
% identity	66
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi_669003 (U20502) calnexin [Glycine max]
Seq. No.	297900
Seq. ID	LIB3150-059-Q1-N1-D12

Method BLASTX
NCBI GI g3983663
BLAST score 554
E value 4.0e-57
Match length 124
% identity 85
NCBI Description (AB011270) importin-beta1 [Oryza sativa]

Seq. No. 297901
Seq. ID LIB3150-059-Q1-N1-D6
Method BLASTN
NCBI GI g899607
BLAST score 50
E value 1.0e-19
Match length 94
% identity 58
NCBI Description Zea mays polyubiquitin (MubC5) mRNA, complete cds

Seq. No. 297902
Seq. ID LIB3150-060-Q1-N1-C2
Method BLASTX
NCBI GI g4056483
BLAST score 146
E value 1.0e-09
Match length 71
% identity 48
NCBI Description (AC005896) hypothetical protein [Arabidopsis thaliana]

Seq. No. 297903
Seq. ID LIB3150-060-Q1-N1-C6
Method BLASTX
NCBI GI g2914700
BLAST score 261
E value 3.0e-23
Match length 58
% identity 84
NCBI Description (AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No. 297904
Seq. ID LIB3150-060-Q1-N1-D10
Method BLASTX
NCBI GI g1184776
BLAST score 177
E value 1.0e-17
Match length 61
% identity 85
NCBI Description (U45857) cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPC4 [Zea mays]

Seq. No. 297905
Seq. ID LIB3150-060-Q1-N1-F8
Method BLASTX
NCBI GI g2642213
BLAST score 159
E value 2.0e-14
Match length 45

% identity 93
NCBI Description (AF030385) nitrate-induced NOI protein [Zea mays]
>gi_2895781 (AF045033) nitrate-induced NOI protein [Zea mays]

Seq. No. 297906
Seq. ID LIB3150-060-Q1-N1-H10
Method BLASTX
NCBI GI g1184776
BLAST score 151
E value 4.0e-10
Match length 58
% identity 47
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
GAPC4 [Zea mays]

Seq. No. 297907
Seq. ID LIB3150-061-Q1-N1-D1
Method BLASTX
NCBI GI g135398
BLAST score 272
E value 2.0e-34
Match length 94
% identity 76
NCBI Description TUBULIN ALPHA-1 CHAIN >gi_82731_pir_S15773 tubulin alpha-1
chain - maize >gi_22147_emb_CAA33734_ (X15704)
alpha1-tubulin [Zea mays]

Seq. No. 297908
Seq. ID LIB3150-063-P2-K1-A8
Method BLASTN
NCBI GI g1575127
BLAST score 92
E value 2.0e-44
Match length 136
% identity 92
NCBI Description Zea mays luminal binding protein cBiPe2 mRNA, complete cds

Seq. No. 297909
Seq. ID LIB3150-063-P2-K1-H6
Method BLASTN
NCBI GI g1037129
BLAST score 59
E value 8.0e-25
Match length 83
% identity 93
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 297910
Seq. ID LIB3150-064-P1-N1-A5
Method BLASTX
NCBI GI g1708107
BLAST score 312
E value 1.0e-28
Match length 87
% identity 76

NCBI Description HISTONE H2B >gi_473605 (U08226) histone H2B [Zea mays]

Seq. No. 297911
Seq. ID LIB3150-064-P1-N1-B8
Method BLASTX
NCBI GI g2828280
BLAST score 400
E value 5.0e-39
Match length 101
% identity 72
NCBI Description (AL021687) putative protein [Arabidopsis thaliana]
>gi_2832633_emb_CAA16762_ (AL021711) putative protein
[Arabidopsis thaliana]

Seq. No. 297912
Seq. ID LIB3150-064-P1-N1-H1
Method BLASTX
NCBI GI g113460
BLAST score 291
E value 3.0e-26
Match length 84
% identity 70
NCBI Description ADP,ATP CARRIER PROTEIN 2 PRECURSOR (ADP/ATP TRANSLOCASE 2)
(ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2)
>gi_100851_pir_S16568 ADP,ATP carrier protein precursor -
maize >gi_22164_emb_CAA41812_ (X59086) adenine nucleotide
translocator [Zea mays]

Seq. No. 297913
Seq. ID LIB3150-064-P2-K1-B5
Method BLASTN
NCBI GI g902585
BLAST score 38
E value 3.0e-12
Match length 46
% identity 96
NCBI Description Zea mays clone MubG9 ubiquitin gene, complete cds

Seq. No. 297914
Seq. ID LIB3150-064-P2-K1-B7
Method BLASTN
NCBI GI g2340954
BLAST score 193
E value 1.0e-104
Match length 213
% identity 98
NCBI Description Z.mays ESR3g2 gene, clone L42a4

Seq. No. 297915
Seq. ID LIB3150-064-P2-K1-D8
Method BLASTX
NCBI GI g4519539
BLAST score 153
E value 5.0e-14
Match length 124
% identity 39
NCBI Description (AB016256) NAD-dependent sorbitol dehydrogenase [Malus

domestica]

Seq. No. 297916
Seq. ID LIB3150-064-P2-K1-F4
Method BLASTX
NCBI GI g2829869
BLAST score 249
E value 3.0e-21
Match length 69
% identity 65
NCBI Description (AC002396) pyruvate dehydrogenase E1 alpha subunit
[Arabidopsis thaliana]

Seq. No. 297917
Seq. ID LIB3150-064-P2-K1-G2
Method BLASTN
NCBI GI g1184775
BLAST score 40
E value 2.0e-13
Match length 72
% identity 89
NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC4
(gpc4) mRNA, complete cds

Seq. No. 297918
Seq. ID LIB3150-064-P2-K1-H6
Method BLASTN
NCBI GI g606969
BLAST score 35
E value 2.0e-10
Match length 71
% identity 87
NCBI Description Arabidopsis thaliana cytoplasmic ribosomal protein L18
mRNA, complete cds

Seq. No. 297919
Seq. ID LIB3150-065-P2-K1-A3
Method BLASTX
NCBI GI g1321661
BLAST score 154
E value 3.0e-10
Match length 39
% identity 79
NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]

Seq. No. 297920
Seq. ID LIB3150-065-P2-K1-B10
Method BLASTN
NCBI GI g3851000
BLAST score 151
E value 2.0e-79
Match length 267
% identity 90
NCBI Description Zea mays pyruvate dehydrogenase E1 beta subunit isoform 2
mRNA, nuclear gene encoding mitochondrial protein, complete
cds

Seq. No. 297921
Seq. ID LIB3150-065-P2-K1-B7
Method BLASTX
NCBI GI g2459446
BLAST score 232
E value 1.0e-19
Match length 90
% identity 52
NCBI Description (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No. 297922
Seq. ID LIB3150-065-P2-K1-C11
Method BLASTX
NCBI GI g1350983
BLAST score 211
E value 1.0e-16
Match length 86
% identity 51
NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)

Seq. No. 297923
Seq. ID LIB3150-065-P2-K1-C6
Method BLASTN
NCBI GI g168584
BLAST score 80
E value 5.0e-37
Match length 215
% identity 92
NCBI Description Corn pyruvate,orthophosphate dikinase gene, exons 2-19

Seq. No. 297924
Seq. ID LIB3150-065-P2-K1-D5
Method BLASTX
NCBI GI g2129553
BLAST score 319
E value 2.0e-29
Match length 79
% identity 72
NCBI Description calcium-dependent protein kinase 6 - Arabidopsis thaliana

Seq. No. 297925
Seq. ID LIB3150-065-P2-K1-F4
Method BLASTN
NCBI GI g168419
BLAST score 82
E value 2.0e-38
Match length 155
% identity 89
NCBI Description Maize (Z.mays) aldolase mRNA, complete cds

Seq. No. 297926
Seq. ID LIB3150-065-P2-K1-G3
Method BLASTN
NCBI GI g1917018
BLAST score 80
E value 6.0e-37

Match length 136
% identity 90
NCBI Description Zea mays ribosomal protein S6 RPS6-1 (rps6-1) mRNA, complete cds

Seq. No. 297927
Seq. ID LIB3150-065-P2-K1-G8
Method BLASTN
NCBI GI g22312
BLAST score 52
E value 2.0e-20
Match length 180
% identity 83
NCBI Description Maize ABA-inducible gene for glycine-rich protein (ABA = abscisic acid)

Seq. No. 297928
Seq. ID LIB3150-066-P1-N1-A10
Method BLASTX
NCBI GI g2181180
BLAST score 144
E value 3.0e-09
Match length 80
% identity 35
NCBI Description (Z84377) xylosidase [Aspergillus niger]

Seq. No. 297929
Seq. ID LIB3150-066-P1-N1-B3
Method BLASTX
NCBI GI g1184774
BLAST score 326
E value 1.0e-30
Match length 69
% identity 91
NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]

Seq. No. 297930
Seq. ID LIB3150-066-P1-N1-F1
Method BLASTN
NCBI GI g1276936
BLAST score 52
E value 1.0e-20
Match length 76
% identity 92
NCBI Description Zea mays USDA Ames 8212 ITS1, 5.8S ribosomal RNA, ITS2

Seq. No. 297931
Seq. ID LIB3150-066-P1-N1-G4
Method BLASTX
NCBI GI g1658315
BLAST score 347
E value 7.0e-33
Match length 99
% identity 69
NCBI Description (Y08988) osr40g3 [Oryza sativa]

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Seq. No. 297932
Seq. ID LIB3150-066-P2-K1-A6
Method BLASTX
NCBI GI g1498064
BLAST score 251
E value 2.0e-21
Match length 81
% identity 63
NCBI Description (U64825) AtE1 [Arabidopsis thaliana]

Seq. No. 297933
Seq. ID LIB3150-066-P2-K1-G10
Method BLASTN
NCBI GI g2282583
BLAST score 84
E value 2.0e-39
Match length 152
% identity 89
NCBI Description Zea mays elongation factor 1-alpha (EF1-A) mRNA, complete cds

Seq. No. 297934
Seq. ID LIB3150-066-P2-K1-G4
Method BLASTN
NCBI GI g296203
BLAST score 43
E value 6.0e-15
Match length 79
% identity 89
NCBI Description P. miliaceum mRNA for alanine aminotransferase

Seq. No. 297935
Seq. ID LIB3150-066-P2-K1-H2
Method BLASTX
NCBI GI g464707
BLAST score 283
E value 3.0e-25
Match length 70
% identity 77
NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi_480908_pir_S37496 ribosomal protein S18.A - Arabidopsis thaliana
>gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana]
>gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana]
>gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana]
>gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No. 297936
Seq. ID LIB3150-067-P1-N1-E2

Method BLASTX
NCBI GI g82512
BLAST score 171
E value 2.0e-12
Match length 37
% identity 47
NCBI Description ubiquitin precursor - rice (fragment)
>gi_218189_dbj_BAA02241_ (D12776) poly-ubiquitin [Oryza sativa]

Seq. No. 297937
Seq. ID LIB3150-067-P1-N1-G4
Method BLASTN
NCBI GI g22176
BLAST score 163
E value 1.0e-86
Match length 289
% identity 89
NCBI Description Z.mays P gene

Seq. No. 297938
Seq. ID LIB3150-067-P2-K1-A6
Method BLASTX
NCBI GI g2511531
BLAST score 197
E value 9.0e-16
Match length 49
% identity 73
NCBI Description (AF008120) alpha tubulin 1 [Eleusine indica]
>gi_3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1 [Eleusine indica]

Seq. No. 297939
Seq. ID LIB3150-067-P2-K1-B12
Method BLASTN
NCBI GI g2286150
BLAST score 151
E value 3.0e-79
Match length 331
% identity 85
NCBI Description Zea mays translation initiation factor (eIF-4A) mRNA, complete cds

Seq. No. 297940
Seq. ID LIB3150-067-P2-K1-D4
Method BLASTN
NCBI GI g168482
BLAST score 95
E value 3.0e-46
Match length 159
% identity 91
NCBI Description Corn starch branching enzyme II mRNA, complete cds

Seq. No. 297941
Seq. ID LIB3150-067-P2-K1-D6
Method BLASTN
NCBI GI g2668741

BLAST score 165
E value 7.0e-88
Match length 248
% identity 92
NCBI Description Zea mays glycine-rich RNA binding protein (GRP) mRNA, complete cds

Seq. No. 297942
Seq. ID LIB3150-067-P2-K1-F3
Method BLASTX
NCBI GI g1172836
BLAST score 169
E value 3.0e-12
Match length 46
% identity 76
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi_496272 (L16787) small ras-related protein [Nicotiana tabacum]

Seq. No. 297943
Seq. ID LIB3150-067-P2-K1-G2
Method BLASTX
NCBI GI g4096786
BLAST score 168
E value 7.0e-12
Match length 35
% identity 94
NCBI Description (U39958) NADP-malic enzyme [Zea mays]

Seq. No. 297944
Seq. ID LIB3150-068-P1-N1-B6
Method BLASTX
NCBI GI g44467099
BLAST score 221
E value 4.0e-18
Match length 72
% identity 71
NCBI Description (AL035538) glycine hydroxymethyltransferase like protein [Arabidopsis thaliana]

Seq. No. 297945
Seq. ID LIB3150-068-P1-N1-C2
Method BLASTX
NCBI GI g1184774
BLAST score 271
E value 5.0e-24
Match length 74
% identity 78
NCBI Description (U45856) cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]

Seq. No. 297946
Seq. ID LIB3150-068-P1-N1-C5
Method BLASTX
NCBI GI g1709619
BLAST score 280
E value 5.0e-25
Match length 57

% identity 95
NCBI Description PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) /
DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE
(GLYCOSYLATION SITE-BINDING CHAIN) (GSBP)
>gi_2146814_pir_S69181 protein disulfide isomerase (EC
5.3.4.1) precursor - maize >gi_625148 (L39014) protein
disulfide isomerase [Zea mays]

Seq. No. 297947
Seq. ID LIB3150-068-P1-N1-F4
Method BLASTX
NCBI GI g1835729
BLAST score 159
E value 8.0e-11
Match length 38
% identity 87
NCBI Description (U86017) ribosomal protein [Oryza sativa]

Seq. No. 297948
Seq. ID LIB3150-068-P1-N1-F8
Method BLASTX
NCBI GI g136632
BLAST score 250
E value 5.0e-22
Match length 61
% identity 82
NCBI Description UBIQUITIN-ACTIVATING ENZYME E1 1 >gi_100841_pir_A38373
ubiquitin--protein ligase (EC 6.3.2.19) E1 - wheat
>gi_285451_pir_A42873 ubiquitin-activating enzyme E1, UBA1
- Wheat >gi_170780 (M55604) ubiquitin-activating enzyme E1
[Triticum aestivum]

Seq. No. 297949
Seq. ID LIB3150-068-P1-N1-H6
Method BLASTN
NCBI GI g22101
BLAST score 41
E value 6.0e-14
Match length 132
% identity 83
NCBI Description Maize 7SL RNA of signal recognition particle

Seq. No. 297950
Seq. ID LIB3150-068-P2-K1-B11
Method BLASTX
NCBI GI g1350777
BLAST score 237
E value 7.0e-20
Match length 71
% identity 66
NCBI Description 60S RIBOSOMAL PROTEIN L9 >gi_971282_dbj_BAA07209_ (D38012)
ribosomal protein L9 [Oryza sativa]

Seq. No. 297951
Seq. ID LIB3150-068-P2-K1-C7
Method BLASTN
NCBI GI g22144

BLAST score 244
E value 1.0e-135
Match length 260
% identity 98
NCBI Description Maize anaerobically regulated gene for fructose bisphosphate aldolase (EC 4.1.2.13)

Seq. No. 297952
Seq. ID LIB3150-068-P2-K1-F12
Method BLASTX
NCBI GI g1350777
BLAST score 234
E value 1.0e-19
Match length 53
% identity 85
NCBI Description 60S RIBOSOMAL PROTEIN L9 >gi_971282_dbj_BAA07209_ (D38012)
ribosomal protein L9 [Oryza sativa]

Seq. No. 297953
Seq. ID LIB3150-068-P2-K1-G2
Method BLASTX
NCBI GI g1707017
BLAST score 272
E value 6.0e-24
Match length 66
% identity 74
NCBI Description (U78721) RNA helicase isolog [Arabidopsis thaliana]

Seq. No. 297954
Seq. ID LIB3150-068-P2-K1-H3
Method BLASTX
NCBI GI g556401
BLAST score 146
E value 3.0e-09
Match length 55
% identity 51
NCBI Description (M28159) glutelin [Oryza sativa]

Seq. No. 297955
Seq. ID LIB3150-068-P2-K1-H8
Method BLASTX
NCBI GI g3970823
BLAST score 288
E value 9.0e-26
Match length 56
% identity 98
NCBI Description (X17555) pyruvate decarboxylase [Zea mays]

Seq. No. 297956
Seq. ID LIB3150-069-P1-N1-B6
Method BLASTX
NCBI GI g118104
BLAST score 184
E value 3.0e-14
Match length 39
% identity 92
NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)

(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
>gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
maize >gi_168461 (M55021) cyclophilin [Zea mays]
>gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 297957
Seq. ID LIB3150-069-P1-N1-D8
Method BLASTX
NCBI GI g232031
BLAST score 142
E value 3.0e-09
Match length 36
% identity 75
NCBI Description ELONGATION FACTOR 1 BETA' >gi_322851_pir_S29224
translation elongation factor eEF-1 beta' chain - rice
>gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta'
[Oryza sativa]

Seq. No. 297958
Seq. ID LIB3150-069-P1-N1-F1
Method BLASTX
NCBI GI g2244990
BLAST score 187
E value 4.0e-14
Match length 37
% identity 100
NCBI Description (Z97340) similarity to LIM homeobox protein -
Caenorhabditis [Arabidopsis thaliana]

Seq. No. 297959
Seq. ID LIB3150-069-P1-N1-F7
Method BLASTX
NCBI GI g1350783
BLAST score 160
E value 5.0e-11
Match length 97
% identity 39
NCBI Description RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR
>gi_282883_pir_S27756 receptor-like protein kinase
precursor - Arabidopsis thaliana >gi_166850 (M84660)
receptor-like protein kinase [Arabidopsis thaliana]
>gi_2842492_emb_CAA16889_ (AL021749) receptor-like protein
kinase 5 precursor (RLK5) [Arabidopsis thaliana]

Seq. No. 297960
Seq. ID LIB3150-069-P1-N1-H6
Method BLASTX
NCBI GI g1173055
BLAST score 152
E value 4.0e-22
Match length 94
% identity 60
NCBI Description 60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir_S42497
ribosomal protein L11.e - alfalfa >gi_1076504_pir_S51819
RL5 ribosomal protein - alfalfa >gi_463252_emb_CAA55090_
(X78284) RL5 ribosomal protein [Medicago sativa]

Seq. No. 297961
Seq. ID LIB3150-069-P2-K1-C11
Method BLASTN
NCBI GI g1037129
BLAST score 58
E value 4.0e-24
Match length 86
% identity 92
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 297962
Seq. ID LIB3150-069-P2-K1-D8
Method BLASTN
NCBI GI g22272
BLAST score 80
E value 4.0e-37
Match length 167
% identity 87
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)

Seq. No. 297963
Seq. ID LIB3150-069-P2-K1-F2
Method BLASTX
NCBI GI g567890
BLAST score 153
E value 5.0e-10
Match length 129
% identity 38
NCBI Description (L37352) beta-galactosidase-complementation protein [Cloning vector]

Seq. No. 297964
Seq. ID LIB3150-069-P2-K1-F4
Method BLASTX
NCBI GI g135417
BLAST score 225
E value 1.0e-18
Match length 74
% identity 66
NCBI Description TUBULIN ALPHA-3 CHAIN >gi_100946_pir_JN0105 tubulin alpha-3 chain - maize >gi_22150_emb_CAA44861 (X63176) Alpha-tubulin #3 [Zea mays] >gi_485377 (M60171) alpha-3 tubulin [Zea mays]

Seq. No. 297965
Seq. ID LIB3150-069-P2-K1-G9
Method BLASTX
NCBI GI g464706
BLAST score 156
E value 2.0e-10
Match length 43
% identity 77
NCBI Description 40S RIBOSOMAL PROTEIN S15 (S12) >gi_1078669_pir_A53793 ribosomal protein S12, cytosolic - Podospora anserina >gi_401841_emb_CAA80805 (Z23267) cytoplasmic ribosomal protein S12 [Podospora anserina]

Seq. No. 297966
 Seq. ID LIB3150-070-P1-N1-B9
 Method BLASTX
 NCBI GI g1084457
 BLAST score 158
 E value 7.0e-11
 Match length 51
 % identity 65
 NCBI Description elongation factor 1-beta - Rice >gi_432368_dbj_BAA04903_ (D23674) elongation factor 1 beta [Oryza sativa]

 Seq. No. 297967
 Seq. ID LIB3150-070-P1-N1-D10
 Method BLASTN
 NCBI GI g829147
 BLAST score 51
 E value 4.0e-20
 Match length 139
 % identity 84
 NCBI Description Z.mays gene for cyclophilin

 Seq. No. 297968
 Seq. ID LIB3150-071-P1-N1-C7
 Method BLASTX
 NCBI GI g82696
 BLAST score 187
 E value 2.0e-14
 Match length 46
 % identity 78
 NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_ (X61121) glycine-rich protein [Zea mays]

 Seq. No. 297969
 Seq. ID LIB3150-071-P1-N1-D11
 Method BLASTX
 NCBI GI g399414
 BLAST score 245
 E value 7.0e-21
 Match length 78
 % identity 65
 NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
 >gi_322865_pir_JC1454 translation elongation factor eEF-1 alpha chain - wheat >gi_170776 (M90077) translation elongation factor 1 alpha-subunit [Triticum aestivum]
 >gi_949878_emb_CAA90651_ (Z50789) elongation factor 1-alpha [Hordeum vulgare]

 Seq. No. 297970
 Seq. ID LIB3150-071-P1-N1-D6
 Method BLASTX
 NCBI GI g1184776
 BLAST score 265
 E value 2.0e-23
 Match length 76
 % identity 75
 NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC4 [Zea mays]

Seq. No. 297971
Seq. ID LIB3150-071-P1-N1-E12
Method BLASTN
NCBI GI g22172
BLAST score 61
E value 6.0e-26
Match length 61
% identity 100
NCBI Description Maize ATP2 mRNA for mitochondrial ATP synthase beta subunit

Seq. No. 297972
Seq. ID LIB3150-071-P1-N1-E2
Method BLASTX
NCBI GI g122007
BLAST score 142
E value 5.0e-09
Match length 38
% identity 79
NCBI Description HISTONE H2A >gi_100161_pir_S11498 histone H2A - parsley
>gi_20448_emb_CAA37828_ (X53831) H2A histone protein (AA 1
- 149) [Petroselinum crispum]

Seq. No. 297973
Seq. ID LIB3150-071-P1-N1-E9
Method BLASTX
NCBI GI g4038461
BLAST score 187
E value 3.0e-14
Match length 72
% identity 51
NCBI Description (AF107772) TcSTI1 [Trypanosoma cruzi]

Seq. No. 297974
Seq. ID LIB3150-071-P1-N1-F1
Method BLASTX
NCBI GI g2723473
BLAST score 155
E value 2.0e-23
Match length 94
% identity 67
NCBI Description (D89726) defender against apoptotic death 1 protein [Oryza sativa] >gi_2723883_dbj_BAA24104_ (D89727) defender against apoptotic death 1 protein [Oryza sativa]

Seq. No. 297975
Seq. ID LIB3150-071-P1-N1-F2
Method BLASTX
NCBI GI g2642158
BLAST score 221
E value 5.0e-18
Match length 83
% identity 55
NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No. 297976

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Seq. ID LIB3150-071-P1-N1-F7
Method BLASTX
NCBI GI g3122071
BLAST score 419
E value 2.0e-42
Match length 106
% identity 84
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
>gi_2130148_pir_S66339 translation elongation factor eEF-1
alpha chain - maize >gi_1321656_dbj_BAA08249_ (D45408)
alpha subunit of tlation elongation factor 1 [Zea mays]

Seq. No. 297977
Seq. ID LIB3150-071-P1-N1-F8
Method BLASTN
NCBI GI g4185305
BLAST score 44
E value 1.0e-15
Match length 60
% identity 48
NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
(sz22-21) gene, complete cds; retrotransposon Opie-2 gag
protein, polyprotein, and copia protein genes, complete
cds; and unknown genes

Seq. No. 297978
Seq. ID LIB3150-071-P1-N1-G10
Method BLASTX
NCBI GI g121446
BLAST score 251
E value 1.0e-21
Match length 70
% identity 76
NCBI Description FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE PRECURSOR
(FD-GOGAT) >gi_100877_pir_A38596 glutamate synthase
(ferredoxin) (EC 1.4.7.1) - maize >gi_168477 (M59190)
ferredoxin-dependent glutamate synthase [Zea mays]

Seq. No. 297979
Seq. ID LIB3150-072-P2-K1-A9
Method BLASTX
NCBI GI g3779021
BLAST score 149
E value 1.0e-09
Match length 87
% identity 37
NCBI Description (AC005171) putative reverse transcriptase [Arabidopsis
thaliana]

Seq. No. 297980
Seq. ID LIB3150-072-P2-K1-D3
Method BLASTX
NCBI GI g2191131
BLAST score 209
E value 2.0e-16
Match length 87
% identity 47

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NCBI Description (AF007269) A_IG002N01.8 gene product [Arabidopsis thaliana]
Seq. No. 297981
Seq. ID LIB3150-073-P1-N1-A11
Method BLASTX
NCBI GI g3342821
BLAST score 188
E value 2.0e-21
Match length 90
% identity 56
NCBI Description (AF076954) eukaryotic translation initiation factor small subunit [Zea mays]
Seq. No. 297982
Seq. ID LIB3150-073-P1-N1-E10
Method BLASTX
NCBI GI g1350720
BLAST score 235
E value 8.0e-20
Match length 73
% identity 63
NCBI Description 60S RIBOSOMAL PROTEIN L32
Seq. No. 297983
Seq. ID LIB3150-073-P1-N1-E5
Method BLASTX
NCBI GI g3413700
BLAST score 168
E value 2.0e-12
Match length 37
% identity 86
NCBI Description (AC004747) putative YME1 protein [Arabidopsis thaliana]
Seq. No. 297984
Seq. ID LIB3150-073-P1-N1-E8
Method BLASTX
NCBI GI g1326372
BLAST score 153
E value 2.0e-10
Match length 68
% identity 51
NCBI Description (U58750) Similar to Histone. [Caenorhabditis elegans]
Seq. No. 297985
Seq. ID LIB3150-073-P1-N1-F3
Method BLASTX
NCBI GI g1381676
BLAST score 236
E value 9.0e-20
Match length 73
% identity 68
NCBI Description (U58853) small GTP-binding protein [Glycine max]
Seq. No. 297986
Seq. ID LIB3150-073-P1-N1-G2
Method BLASTX
NCBI GI g2244834

BLAST score 165
E value 1.0e-11
Match length 41
% identity 66
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 297987
Seq. ID LIB3150-073-P1-N1-G5
Method BLASTX
NCBI GI g3608481
BLAST score 272
E value 3.0e-24
Match length 68
% identity 75
NCBI Description (AF088913) ribosomal protein L27a [Petunia x hybrida]

Seq. No. 297988
Seq. ID LIB3150-073-P2-K1-A1
Method BLASTN
NCBI GI g644491
BLAST score 56
E value 8.0e-23
Match length 152
% identity 85
NCBI Description Corn mRNA for elongation factor 1A

Seq. No. 297989
Seq. ID LIB3150-073-P2-K1-A11
Method BLASTX
NCBI GI g1172816
BLAST score 194
E value 7.0e-15
Match length 70
% identity 60
NCBI Description 60S RIBOSOMAL PROTEIN L11A (L16A) >gi_624938_<emb>CAA57395</emb>_<X>81799</X> ribosomal protein L16 [Arabidopsis thaliana]

Seq. No. 297990
Seq. ID LIB3150-073-P2-K1-A7
Method BLASTX
NCBI GI g136063
BLAST score 261
E value 9.0e-23
Match length 53
% identity 100
NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
>gi_68426_pir_ISZMT triose-phosphate isomerase (EC
5.3.1.1) - maize >gi_168647 (L00371) triosephosphate
isomerase 1 [Zea mays] >gi_217974_dbj_BAA00009_ (D00012)
triosephosphate isomerase [Zea mays]

Seq. No. 297991
Seq. ID LIB3150-073-P2-K1-A9
Method BLASTX
NCBI GI g1172874
BLAST score 145
E value 5.0e-09

Match length 102
% identity 35
NCBI Description DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR
>gi_479589_pir_S34823 dehydration-induced protein RD22 -
Arabidopsis thaliana >gi_391608_dbj_BAA01546 (D10703) rd22
[Arabidopsis thaliana] >gi_447134_prf_1913421A rd22 gene
[Arabidopsis thaliana]

Seq. No. 297992
Seq. ID LIB3150-073-P2-K1-B10
Method BLASTN
NCBI GI g4185305
BLAST score 43
E value 6.0e-15
Match length 207
% identity 81
NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
(sz22-21) gene, complete cds; retrotransposon Opie-2 gag
protein, polyprotein, and copia protein genes, complete
cds; and unknown genes

Seq. No. 297993
Seq. ID LIB3150-073-P2-K1-B3
Method BLASTX
NCBI GI g3745759
BLAST score 195
E value 6.0e-15
Match length 56
% identity 70
NCBI Description Chain B, X-Ray Structure Of The Nucleosome Core Particle At
2.8 A Resolution >gi_3745763_pdb_1AOI_F Chain F, X-Ray
Structure Of The Nucleosome Core Particle At 2.8 A
Resolution

Seq. No. 297994
Seq. ID LIB3150-073-P2-K1-B8
Method BLASTN
NCBI GI g2286150
BLAST score 263
E value 1.0e-146
Match length 275
% identity 99
NCBI Description Zea mays translation initiation factor (eIF-4A) mRNA,
complete cds

Seq. No. 297995
Seq. ID LIB3150-073-P2-K1-C4
Method BLASTX
NCBI GI g2182029
BLAST score 233
E value 2.0e-19
Match length 89
% identity 57
NCBI Description (Y13437) shaggy-like kinase etha (OSKetha) [Oryza sativa]

Seq. No. 297996
Seq. ID LIB3150-073-P2-K1-C9

Method BLASTN
NCBI GI g22324
BLAST score 71
E value 1.0e-31
Match length 151
% identity 87
NCBI Description Z. mays mRNA for H2B histone (clone cH2B221)

Seq. No. 297997
Seq. ID LIB3150-073-P2-K1-F11
Method BLASTN
NCBI GI g602605
BLAST score 72
E value 3.0e-32
Match length 254
% identity 63
NCBI Description Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin

Seq. No. 297998
Seq. ID LIB3150-074-P1-N1-D2
Method BLASTX
NCBI GI g1321661
BLAST score 186
E value 3.0e-14
Match length 52
% identity 71
NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]

Seq. No. 297999
Seq. ID LIB3150-074-P1-N1-E2
Method BLASTX
NCBI GI g3126967
BLAST score 358
E value 1.0e-34
Match length 99
% identity 14
NCBI Description (AF061807) polyubiquitin [Elaeagnus umbellata]

Seq. No. 298000
Seq. ID LIB3150-074-P1-N1-F12
Method BLASTN
NCBI GI g642120
BLAST score 48
E value 3.0e-18
Match length 76
% identity 91
NCBI Description Oryza sativa small GTP-binding protein (ORRab-2) mRNA, complete cds

Seq. No. 298001
Seq. ID LIB3150-074-P1-N1-H6
Method BLASTX
NCBI GI g2144183
BLAST score 156
E value 5.0e-11
Match length 53
% identity 53

NCBI Description DNA-directed RNA polymerase (EC 2.7.7.6) chain III - Ecotype Columbia >gi_1184686 (U35049) RNA polymerase I (A) and III(C) 14 kDa subunit [Arabidopsis thaliana]
>gi_1184688 (U35050) Arabidopsis thaliana RNA polymerase I (A) and III(C) 14 kDa subunit [Arabidopsis thaliana]
>gi_3980382 (AC004561) RNA polymerase I (A) and III(C) 14 kDa subunit (AtRPAC14) [Arabidopsis thaliana]

Seq. No. 298002
Seq. ID LIB3150-074-P2-K1-G7
Method BLASTN
NCBI GI g602605
BLAST score 43
E value 5.0e-15
Match length 75
% identity 89
NCBI Description Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin

Seq. No. 298003
Seq. ID LIB3150-074-P2-K1-H4
Method BLASTN
NCBI GI g902585
BLAST score 67
E value 2.0e-29
Match length 219
% identity 83
NCBI Description Zea mays clone MubG9 ubiquitin gene, complete cds

Seq. No. 298004
Seq. ID LIB3150-074-P2-K1-H7
Method BLASTN
NCBI GI g393400
BLAST score 71
E value 8.0e-32
Match length 156
% identity 85
NCBI Description Z.mays mRNA for alpha-tubulin

Seq. No. 298005
Seq. ID LIB3150-075-P1-N1-D1
Method BLASTX
NCBI GI g4588906
BLAST score 195
E value 2.0e-15
Match length 49
% identity 80
NCBI Description (AF118149) ribosomal protein S7 [Secale cereale]

Seq. No. 298006
Seq. ID LIB3150-075-P1-N1-E10
Method BLASTN
NCBI GI g540534
BLAST score 58
E value 6.0e-24
Match length 82
% identity 93
NCBI Description Rice mRNA for q group of receptor for activated C-kinase,

complete cds

Seq. No. 298007
Seq. ID LIB3150-075-P1-N1-E7
Method BLASTX
NCBI GI g1184774
BLAST score 165
E value 2.0e-20
Match length 59
% identity 92
NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
GAPC3 [Zea mays]

Seq. No. 298008
Seq. ID LIB3150-075-P1-N1-F7
Method BLASTX
NCBI GI g1053047
BLAST score 301
E value 1.0e-27
Match length 68
% identity 90
NCBI Description (U38425) histone H3 [Glycine max] >gi_1053049 (U38426)
histone H3 [Glycine max] >gi_1053051 (U38427) histone H3
[Glycine max]

Seq. No. 298009
Seq. ID LIB3150-075-P1-N1-G7
Method BLASTX
NCBI GI g729676
BLAST score 204
E value 2.0e-18
Match length 75
% identity 72
NCBI Description HISTONE H3.1 >gi_542444_pir_S41499 histone H3.1 -
Tetrahymena thermophila (SGC5) >gi_161788 (M87304) histone
H3 [Tetrahymena thermophila] >gi_161790 (M87504) histone H3
[Tetrahymena thermophila]

Seq. No. 298010
Seq. ID LIB3150-075-P2-N2-A3
Method BLASTX
NCBI GI g113621
BLAST score 332
E value 5.0e-31
Match length 67
% identity 97
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
>gi_68196_pir_ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
[Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
bisphosphate aldolase [Zea mays] >gi_225624_prf_1307278A
cytoplasmic aldolase [Zea mays]

Seq. No. 298011
Seq. ID LIB3150-075-P2-N2-B1
Method BLASTX
NCBI GI g2982289

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BLAST score 397
E value 1.0e-38
Match length 78
% identity 97
NCBI Description (AF051229) 60S ribosomal protein L17 [Picea mariana]

Seq. No. 298012
Seq. ID LIB3150-075-P2-N2-B3
Method BLASTN
NCBI GI g22272
BLAST score 140
E value 6.0e-73
Match length 219
% identity 91
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)

Seq. No. 298013
Seq. ID LIB3150-075-P2-N2-D1
Method BLASTX
NCBI GI g2507281
BLAST score 246
E value 1.0e-24
Match length 66
% identity 91
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_(X97380) atran2 [Arabidopsis thaliana]

Seq. No. 298014
Seq. ID LIB3150-075-P2-N2-D8
Method BLASTX
NCBI GI g401238
BLAST score 536
E value 4.0e-55
Match length 131
% identity 82
NCBI Description UBIQUITIN-ACTIVATING ENZYME E1 3 >gi_170686 (M90664) ubiquitin activating enzyme [Triticum aestivum]

Seq. No. 298015
Seq. ID LIB3150-075-P2-N2-F2
Method BLASTN
NCBI GI g22100
BLAST score 33
E value 3.0e-09
Match length 57
% identity 89
NCBI Description Z.mays 27kDa zein locus DNA

Seq. No. 298016
Seq. ID LIB3150-075-P2-N2-H10
Method BLASTX
NCBI GI g4220445
BLAST score 320
E value 3.0e-32
Match length 132
% identity 22
NCBI Description (AC006216) Similar to gi_3004555 F19F24.14 salt inducible

protein homolog from *Arabidopsis thaliana* BAC gb_AC003673.
[*Arabidopsis thaliana*]

Seq. No. 298017
Seq. ID LIB3150-075-P2-N2-H11
Method BLASTX
NCBI GI g4220445
BLAST score 171
E value 1.0e-12
Match length 73
% identity 47
NCBI Description (AC006216) Similar to gi_3004555 F19F24.14 salt inducible protein homolog from *Arabidopsis thaliana* BAC gb_AC003673.
[*Arabidopsis thaliana*]

Seq. No. 298018
Seq. ID LIB3150-075-P2-N2-H12
Method BLASTX
NCBI GI g1730666
BLAST score 169
E value 7.0e-12
Match length 70
% identity 54
NCBI Description HYPOTHETICAL 32.2 KD PROTEIN IN ARE2-SWP73 INTERGENIC REGION >gi_2131968_pir_S63351 hypothetical protein YNR020c - yeast (*Saccharomyces cerevisiae*)
>gi_1302506_emb_CAA96299 (Z71635) ORF YNR020c
[*Saccharomyces cerevisiae*]

Seq. No. 298019
Seq. ID LIB3150-076-P1-N1-F3
Method BLASTX
NCBI GI g4582468
BLAST score 150
E value 7.0e-10
Match length 64
% identity 47
NCBI Description (AC007071) putative 40S ribosomal protein; contains C-terminal domain [*Arabidopsis thaliana*]

Seq. No. 298020
Seq. ID LIB3150-076-P1-N1-G3
Method BLASTX
NCBI GI g1184776
BLAST score 280
E value 4.0e-25
Match length 71
% identity 79
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC4 [*Zea mays*]

Seq. No. 298021
Seq. ID LIB3150-076-P2-N2-A7
Method BLASTX
NCBI GI g3337352
BLAST score 331
E value 4.0e-31

Match length 101
 % identity 66
 NCBI Description (AC004481) putative chromatin structural protein Supt5hp [Arabidopsis thaliana]

 Seq. No. 298022
 Seq. ID LIB3150-076-P2-N2-A9
 Method BLASTN
 NCBI GI g1839582
 BLAST score 47
 E value 9.0e-18
 Match length 63
 % identity 94
 NCBI Description polyubiquitin homolog {clone CHEM 6} [Zea mays=maize, cv. INRA 258, mercuric chloride-treated, leaves, mRNA Partial, 199 nt, segment 1 of 2]

 Seq. No. 298023
 Seq. ID LIB3150-076-P2-N2-C6
 Method BLASTX
 NCBI GI g2117937
 BLAST score 623
 E value 4.0e-65
 Match length 123
 % identity 94
 NCBI Description UDP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose pyrophosphorylase [Hordeum vulgare]

 Seq. No. 298024
 Seq. ID LIB3150-076-P2-N2-E8
 Method BLASTN
 NCBI GI g4185305
 BLAST score 84
 E value 2.0e-39
 Match length 304
 % identity 83
 NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete cds; and unknown genes

 Seq. No. 298025
 Seq. ID LIB3150-076-P2-N2-F1
 Method BLASTX
 NCBI GI g1351974
 BLAST score 390
 E value 8.0e-38
 Match length 105
 % identity 77
 NCBI Description ADP-RIBOSYLATION FACTOR >gi_1076788_pir_S49325
 ADP-ribosylation factor - maize >gi_1076789_pir_S53486
 ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_ (X80042) ADP-ribosylation factor [Zea mays]

 Seq. No. 298026
 Seq. ID LIB3150-076-P2-N2-G4

Method BLASTN
NCBI GI g22312
BLAST score 70
E value 4.0e-31
Match length 97
% identity 94
NCBI Description Maize ABA-inducible gene for glycine-rich protein (ABA = abscisic acid)

Seq. No. 298027
Seq. ID LIB3150-076-P2-N2-H12
Method BLASTX
NCBI GI g2286153
BLAST score 372
E value 9.0e-36
Match length 75
% identity 100
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No. 298028
Seq. ID LIB3150-076-P2-N2-H5
Method BLASTX
NCBI GI g913865
BLAST score 153
E value 1.0e-10
Match length 49
% identity 61
NCBI Description branching enzyme II BEII [Zea mays, cultivar B73, endosperms, Peptide, 738 aa]

Seq. No. 298029
Seq. ID LIB3150-077-P1-N1-A12
Method BLASTX
NCBI GI g4038471
BLAST score 349
E value 5.0e-33
Match length 86
% identity 80
NCBI Description (AF111029) 40S ribosomal protein S27 homolog [Zea mays]

Seq. No. 298030
Seq. ID LIB3150-077-P1-N1-E5
Method BLASTX
NCBI GI g417154
BLAST score 168
E value 2.0e-18
Match length 84
% identity 79
NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir_S25541 heat shock protein 82 - rice (strain Taichung Native One)
>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

Seq. No. 298031
Seq. ID LIB3150-077-P1-N1-E7
Method BLASTX
NCBI GI g122022

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BLAST score 142
E value 8.0e-09
Match length 94
% identity 44
NCBI Description HISTONE H2B >gi_283025_pir_S22323 histone H2B - wheat
>gi_21801_emb_CAA42530_ (X59873) histone H2B [Triticum aestivum]

Seq. No. 298032
Seq. ID LIB3150-077-P1-N1-F2
Method BLASTX
NCBI GI g3294469
BLAST score 165
E value 2.0e-21
Match length 101
% identity 63
NCBI Description (U89342) phosphoglucomutase 2 [Zea mays]

Seq. No. 298033
Seq. ID LIB3150-077-P1-N1-F4
Method BLASTX
NCBI GI g4567275
BLAST score 248
E value 8.0e-27
Match length 108
% identity 61
NCBI Description (AC006841) hypothetical protein [Arabidopsis thaliana]

Seq. No. 298034
Seq. ID LIB3150-077-P1-N1-G3
Method BLASTN
NCBI GI g3015620
BLAST score 55
E value 3.0e-22
Match length 291
% identity 80
NCBI Description Zea mays low molecular weight heat shock protein precursor (hsp22) mRNA, nuclear gene encoding mitochondrial protein, complete cds

Seq. No. 298035
Seq. ID LIB3150-077-P1-N1-H8
Method BLASTX
NCBI GI g119355
BLAST score 340
E value 5.0e-32
Match length 95
% identity 77
NCBI Description ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
>gi_100869_pir_S16257 phosphopyruvate hydratase (EC
4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
[Zea mays]

Seq. No. 298036
Seq. ID LIB3150-077-P2-N2-C4
Method BLASTN

NCBI GI g22272
BLAST score 99
E value 2.0e-48
Match length 205
% identity 88
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)

Seq. No. 298037
Seq. ID LIB3150-077-P2-N2-E2
Method BLASTN
NCBI GI g1808693
BLAST score 132
E value 5.0e-68
Match length 224
% identity 90
NCBI Description S.staphianus pSD.34 mRNA

Seq. No. 298038
Seq. ID LIB3150-077-P2-N2-E5
Method BLASTX
NCBI GI g118104
BLAST score 547
E value 3.0e-56
Match length 121
% identity 87
NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
>gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
maize >gi_168461 (M55021) cyclophilin [Zea mays]
>gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 298039
Seq. ID LIB3150-077-P2-N2-E6
Method BLASTX
NCBI GI g1185556
BLAST score 159
E value 2.0e-11
Match length 37
% identity 92
NCBI Description (U45859) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No. 298040
Seq. ID LIB3150-077-P2-N2-F9
Method BLASTN
NCBI GI g1037129
BLAST score 191
E value 1.0e-103
Match length 219
% identity 65
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298041
Seq. ID LIB3150-077-P2-N2-G9
Method BLASTX
NCBI GI g2865661

BLAST score	146
E value	2.0e-09
Match length	55
% identity	58
NCBI Description	(AF045548) alcohol dehydrogenase 1 [Tripsacum dactyloides]
Seq. No.	298042
Seq. ID	LIB3150-077-P2-N2-H4
Method	BLASTX
NCBI GI	g2511541
BLAST score	287
E value	7.0e-26
Match length	77
% identity	73
NCBI Description	(AF020787) DNA-binding protein GBP16 [Oryza sativa]
Seq. No.	298043
Seq. ID	LIB3150-078-P1-N1-A8
Method	BLASTX
NCBI GI	g3334138
BLAST score	152
E value	2.0e-10
Match length	41
% identity	63
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi_669003 (U20502) calnexin [Glycine max]
Seq. No.	298044
Seq. ID	LIB3150-078-P1-N1-B6
Method	BLASTX
NCBI GI	g1351904
BLAST score	288
E value	2.0e-26
Match length	70
% identity	83
NCBI Description	ASPARTOKINASE 1 / HOMOSERINE DEHYDROGENASE 1 CHLOROPLAST PRECURSOR (AK-HSDH 1) (AKHSDH1) >gi_500851 (L33912) aspartate kinase-homoserine dehydrogenase [Zea mays]
Seq. No.	298045
Seq. ID	LIB3150-078-P1-N1-C1
Method	BLASTX
NCBI GI	g4218535
BLAST score	211
E value	3.0e-17
Match length	79
% identity	58
NCBI Description	(AJ010829) GRAB1 protein [Triticum sp.]
Seq. No.	298046
Seq. ID	LIB3150-078-P1-N1-D2
Method	BLASTX
NCBI GI	g3367522
BLAST score	418
E value	4.0e-41
Match length	142
% identity	55

NCBI Description (AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No. 298047
Seq. ID LIB3150-078-P1-N1-F1
Method BLASTX
NCBI GI g112994
BLAST score 321
E value 7.0e-30
Match length 71
% identity 92
NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
>gi_82685_pir_S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
ABA-inducible gene protein [Zea mays]
>gi_226091_prf_1410284A abscisic acid inducible gene [Zea mays]

Seq. No. 298048
Seq. ID LIB3150-078-P1-N1-F3
Method BLASTX
NCBI GI g4432866
BLAST score 147
E value 2.0e-09
Match length 80
% identity 39
NCBI Description (AC006300) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No. 298049
Seq. ID LIB3150-078-P1-N1-F8
Method BLASTX
NCBI GI g2282584
BLAST score 484
E value 7.0e-49
Match length 104
% identity 88
NCBI Description (U76259) elongation factor 1-alpha [Zea mays]

Seq. No. 298050
Seq. ID LIB3150-078-P1-N1-G3
Method BLASTX
NCBI GI g112994
BLAST score 427
E value 3.0e-42
Match length 91
% identity 93
NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
>gi_82685_pir_S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
ABA-inducible gene protein [Zea mays]
>gi_226091_prf_1410284A abscisic acid inducible gene [Zea mays]

Seq. No. 298051
Seq. ID LIB3150-078-P1-N1-H7
Method BLASTN

NCBI GI g303854
BLAST score 54
E value 1.0e-21
Match length 162
% identity 85
NCBI Description Rice mRNA for ribosomal protein L7A, complete cds

Seq. No. 298052
Seq. ID LIB3150-078-P2-N2-A3
Method BLASTX
NCBI GI g4580398
BLAST score 349
E value 6.0e-34
Match length 111
% identity 65
NCBI Description (AC007171) putative protein kinase APK1A [Arabidopsis thaliana]

Seq. No. 298053
Seq. ID LIB3150-078-P2-N2-B8
Method BLASTX
NCBI GI g3747050
BLAST score 328
E value 1.0e-30
Match length 69
% identity 96
NCBI Description (AF093540) ribosomal protein L26 [Zea mays]

Seq. No. 298054
Seq. ID LIB3150-078-P2-N2-B9
Method BLASTN
NCBI GI g3747049
BLAST score 35
E value 1.0e-10
Match length 83
% identity 86
NCBI Description Zea mays ribosomal protein L26 mRNA, partial cds

Seq. No. 298055
Seq. ID LIB3150-078-P2-N2-D5
Method BLASTN
NCBI GI g293886
BLAST score 52
E value 6.0e-21
Match length 96
% identity 89
NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase mRNA, 3' end, (clone GACP3)

Seq. No. 298056
Seq. ID LIB3150-078-P2-N2-D8
Method BLASTN
NCBI GI g21800
BLAST score 106
E value 1.0e-52
Match length 196
% identity 89

NCBI Description T.aestivum L mRNA for histone H2B

Seq. No. 298057
Seq. ID LIB3150-079-P1-N1-A11
Method BLASTX
NCBI GI g113621
BLAST score 163
E value 3.0e-11
Match length 68
% identity 57

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
>gi_68196_pir_ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
[Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
bisphosphate aldolase [Zea mays] >gi_225624_prf_1307278A
cytoplasmic aldolase [Zea mays]

Seq. No. 298058
Seq. ID LIB3150-079-P1-N1-A8
Method BLASTX
NCBI GI g232029
BLAST score 238
E value 3.0e-20
Match length 70
% identity 70

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
>gi_100154_pir_S21989 translation elongation factor eEF-1
alpha chain - carrot >gi_18339_emb_CAA42843_ (X60302)
elongation factor 1A [Daucus carota]

Seq. No. 298059
Seq. ID LIB3150-079-P1-N1-D2
Method BLASTX
NCBI GI g2760349
BLAST score 232
E value 9.0e-20
Match length 68
% identity 14

NCBI Description (U84969) ubiquitin [Arabidopsis thaliana]

Seq. No. 298060
Seq. ID LIB3150-079-P1-N1-E2
Method BLASTX
NCBI GI g1184776
BLAST score 405
E value 2.0e-39
Match length 78
% identity 95

NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
GAPC4 [Zea mays]

Seq. No. 298061
Seq. ID LIB3150-079-P1-N1-E3
Method BLASTX
NCBI GI g4510368
BLAST score 276
E value 2.0e-24

09634016-10200

Match length 131
% identity 56
NCBI Description (AC007017) putative transcription factor E2F5 [Arabidopsis thaliana]

Seq. No. 298062
Seq. ID LIB3150-079-P1-N1-E7
Method BLASTX
NCBI GI g730558
BLAST score 225
E value 6.0e-28
Match length 96
% identity 74
NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi_1076636_pir_S48027 ribosomal protein L34 - common tobacco >gi_2129964_pir_S48028 ribosomal protein L34.e, cytosolic - common tobacco >gi_436030 (L27089) 60S ribosomal protein L34 [Nicotiana tabacum] >gi_436032 (L27107) 60S ribosomal protein L34 [Nicotiana tabacum]

Seq. No. 298063
Seq. ID LIB3150-079-P2-N2-A11
Method BLASTN
NCBI GI g3318612
BLAST score 78
E value 6.0e-36
Match length 190
% identity 84
NCBI Description Zea mays mRNA for mitochondrial phosphate transporter, complete cds

Seq. No. 298064
Seq. ID LIB3150-079-P2-N2-B1
Method BLASTN
NCBI GI g416263
BLAST score 37
E value 2.0e-11
Match length 65
% identity 89
NCBI Description Rice mRNA for ribosomal protein S28, partial sequence

Seq. No. 298065
Seq. ID LIB3150-079-P2-N2-E4
Method BLASTN
NCBI GI g1213278
BLAST score 60
E value 3.0e-25
Match length 100
% identity 90
NCBI Description Z.mays ZEMb gene

Seq. No. 298066
Seq. ID LIB3150-079-P2-N2-F3
Method BLASTX
NCBI GI g3805847
BLAST score 315
E value 5.0e-29

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Match length 111
% identity 58
NCBI Description (AL031986) putative protein [Arabidopsis thaliana]

Seq. No. 298067
Seq. ID LIB3150-079-P2-N2-H5
Method BLASTN
NCBI GI g886739
BLAST score 70
E value 3.0e-31
Match length 245
% identity 84
NCBI Description Z.mays histone H4 gene

Seq. No. 298068
Seq. ID LIB3150-080-P2-N2-G2
Method BLASTN
NCBI GI g1550813
BLAST score 102
E value 3.0e-50
Match length 181
% identity 90
NCBI Description Z.mays mRNA for acidic ribosomal protein P0

Seq. No. 298069
Seq. ID LIB3150-081-P1-N1-C6
Method BLASTX
NCBI GI g2137285
BLAST score 145
E value 4.0e-09
Match length 75
% identity 40
NCBI Description estrogen-responsive finger protein - mouse
>gi_1088467_dbj_BAA09941_ (D63902) estrogen-responsive
finger protein [Mus musculus]

Seq. No. 298070
Seq. ID LIB3150-081-P1-N1-E1
Method BLASTX
NCBI GI g425194
BLAST score 448
E value 9.0e-45
Match length 87
% identity 99
NCBI Description (L26243) heat shock protein [Spinacia oleracea] >gi_2660772
(AF034618) cytosolic heat shock 70 protein [Spinacia
oleracea]

Seq. No. 298071
Seq. ID LIB3150-081-P1-N1-G2
Method BLASTX
NCBI GI g3913804
BLAST score 260
E value 1.0e-22
Match length 65
% identity 83
NCBI Description HISTONE H2B.3 >gi_577825_emb_CAA49584_ (X69960) H2B histone

[Zea mays]

Seq. No. 298072
Seq. ID LIB3150-081-P1-N1-H3
Method BLASTX
NCBI GI g118104
BLAST score 477
E value 4.0e-48
Match length 98
% identity 91
NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) -
>gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
maize >gi_168461 (M55021) cyclophilin [Zea mays]
>gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 298073
Seq. ID LIB3150-081-P2-N2-D11
Method BLASTN
NCBI GI g168425
BLAST score 186
E value 1.0e-100
Match length 255
% identity 93
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds

Seq. No. 298074
Seq. ID LIB3150-081-P2-N2-F8
Method BLASTX
NCBI GI g520544
BLAST score 251
E value 1.0e-21
Match length 46
% identity 96
NCBI Description (U12195) betaine aldehyde dehydrogenase [Sorghum bicolor]

Seq. No. 298075
Seq. ID LIB3150-082-P1-N1-A5
Method BLASTX
NCBI GI g168586
BLAST score 147
E value 7.0e-10
Match length 43
% identity 70
NCBI Description (M58656) pyruvate,orthophosphate dikinase [Zea mays]

Seq. No. 298076
Seq. ID LIB3150-082-P1-N1-B8
Method BLASTN
NCBI GI g2811133
BLAST score 100
E value 4.0e-49
Match length 189
% identity 88
NCBI Description Zea mays starch synthase isoform zSTSII-1 (zSSIIa) mRNA,
partial cds

Seq. No. 298077
Seq. ID LIB3150-082-P1-N1-C4
Method BLASTX
NCBI GI g168407
BLAST score 173
E value 2.0e-12
Match length 57
% identity 70
NCBI Description (M32984) alcohol dehydrogenase [Zea mays]

Seq. No. 298078
Seq. ID LIB3150-082-P2-N2-B4
Method BLASTN
NCBI GI g829147
BLAST score 44
E value 5.0e-16
Match length 56
% identity 95
NCBI Description Z.mays gene for cyclophilin

Seq. No. 298079
Seq. ID LIB3150-083-P1-N1-A1
Method BLASTN
NCBI GI g1143704
BLAST score 97
E value 3.0e-47
Match length 125
% identity 94
NCBI Description Z.mays mRNA for homeobox 2a protein

Seq. No. 298080
Seq. ID LIB3150-083-P1-N1-A2
Method BLASTX
NCBI GI g126896
BLAST score 340
E value 1.0e-37
Match length 93
% identity 86
NCBI Description MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
>gi_319831_pir_DEPUMW malate dehydrogenase (EC 1.1.1.37)
precursor, mitochondrial - watermelon
>gi_18297_emb_CAA35239_ (X17362) precursor protein (AA -27
to 320) [Citrullus lanatus]

Seq. No. 298081
Seq. ID LIB3150-083-P1-N1-B3
Method BLASTX
NCBI GI g4206112
BLAST score 175
E value 3.0e-13
Match length 71
% identity 61
NCBI Description (AF097662) alpha tubulin [Mesembryanthemum crystallinum]

Seq. No. 298082
Seq. ID LIB3150-083-P1-N1-B5
Method BLASTX

NCBI GI g4206112
BLAST score 159
E value 2.0e-11
Match length 59
% identity 59
NCBI Description (AF097662) alpha tubulin [Mesembryanthemum crystallinum]

Seq. No. 298083
Seq. ID LIB3150-083-P1-N1-C1
Method BLASTX
NCBI GI g1279206
BLAST score 190
E value 1.0e-14
Match length 68
% identity 62
NCBI Description (X97446) alpha-tubulin [Avena sativa]

Seq. No. 298084
Seq. ID LIB3150-083-P1-N1-E11
Method BLASTX
NCBI GI g1883028
BLAST score 231
E value 2.0e-19
Match length 72
% identity 68
NCBI Description (X91511) histone H4 [Diprion pini]

Seq. No. 298085
Seq. ID LIB3150-083-P1-N1-F2
Method BLASTN
NCBI GI g577824
BLAST score 146
E value 1.0e-76
Match length 170
% identity 96
NCBI Description Z.mays gene for H2B histone (gH2B3)

Seq. No. 298086
Seq. ID LIB3150-083-P1-N1-G4
Method BLASTX
NCBI GI g3935184
BLAST score 384
E value 3.0e-37
Match length 115
% identity 65
NCBI Description (AC004557) F17L21.27 [Arabidopsis thaliana]

Seq. No. 298087
Seq. ID LIB3150-083-P1-N1-H8
Method BLASTX
NCBI GI g3122071
BLAST score 304
E value 4.0e-28
Match length 62
% identity 95
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
>gi_2130148_pir_S66339 translation elongation factor eEF-1

alpha chain - maize >gi_1321656_dbj_BAA08249_ (D45408)
alpha subunit of ttranslational elongation factor 1 [Zea mays]

Seq. No. 298088
Seq. ID LIB3150-083-P2-N2-A10
Method BLASTX
NCBI GI g4406372
BLAST score 188
E value 3.0e-14
Match length 43
% identity 77
NCBI Description (AF109156) thiosulfate sulfurtransferase [Datisca glomerata]

Seq. No. 298089
Seq. ID LIB3150-083-P2-N2-C12
Method BLASTN
NCBI GI g1575127
BLAST score 220
E value 1.0e-120
Match length 280
% identity 94
NCBI Description Zea mays luminal binding protein cBiPe2 mRNA, complete cds

Seq. No. 298090
Seq. ID LIB3150-083-P2-N2-D11
Method BLASTN
NCBI GI g531055
BLAST score 64
E value 1.0e-27
Match length 72
% identity 97
NCBI Description Wheat mRNA for protein H2B-6, complete cds

Seq. No. 298091
Seq. ID LIB3150-083-P2-N2-F12
Method BLASTX
NCBI GI g2760321
BLAST score 309
E value 2.0e-28
Match length 108
% identity 59
NCBI Description (AC002130) F1N21.6 [Arabidopsis thaliana]

Seq. No. 298092
Seq. ID LIB3150-083-P2-N2-G11
Method BLASTX
NCBI GI g480450
BLAST score 158
E value 1.0e-10
Match length 34
% identity 91
NCBI Description ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No. 298093

Seq. ID LIB3150-083-P2-N2-H5
Method BLASTN
NCBI GI g2642323
BLAST score 89
E value 2.0e-42
Match length 222
% identity 86
NCBI Description Zea mays profilin (PRO4) mRNA, complete cds

Seq. No. 298094
Seq. ID LIB3150-084-P2-N2-F6
Method BLASTN
NCBI GI g498772
BLAST score 39
E value 1.0e-12
Match length 67
% identity 91
NCBI Description Z.mays (cv DH5xDH7) hsp70-4 mRNA for heat shock protein

Seq. No. 298095
Seq. ID LIB3150-084-P2-N2-G10
Method BLASTX
NCBI GI g1335862
BLAST score 403
E value 2.0e-39
Match length 88
% identity 86
NCBI Description (U42608) clathrin heavy chain [Glycine max]

Seq. No. 298096
Seq. ID LIB3150-085-P1-N1-B3
Method BLASTX
NCBI GI g312179
BLAST score 264
E value 2.0e-33
Match length 81
% identity 95
NCBI Description (X73151) glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays] >gi_1185554 (U45858) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No. 298097
Seq. ID LIB3150-085-P1-N1-D2
Method BLASTX
NCBI GI g2624328
BLAST score 207
E value 2.0e-16
Match length 63
% identity 65
NCBI Description (AJ002894) OsGRP2 [Oryza sativa]

Seq. No. 298098
Seq. ID LIB3150-085-P1-N1-F1
Method BLASTX
NCBI GI g1172833

095547-1001000

BLAST score	249
E value	1.0e-21
Match length	58
% identity	86
NCBI Description	GTP-BINDING NUCLEAR PROTEIN RAN-1 >gi_495729 (L16789) small ras-related protein [Arabidopsis thaliana] >gi_2058278_emb_CAA66047_ (X97379) atranl [Arabidopsis thaliana]
Seq. No.	298099
Seq. ID	LIB3150-085-P1-N1-G1
Method	BLASTN
NCBI GI	g4099507
BLAST score	66
E value	6.0e-29
Match length	141
% identity	87
NCBI Description	Zea mays proliferating cell nuclear antigen (ZmPCNA2) mRNA, complete cds
Seq. No.	298100
Seq. ID	LIB3150-085-P1-N1-G2
Method	BLASTX
NCBI GI	g1262171
BLAST score	203
E value	6.0e-16
Match length	61
% identity	72
NCBI Description	(U21557) phosphoprotein phosphatase 2A, regulatory subunit A [Arabidopsis thaliana]
Seq. No.	298101
Seq. ID	LIB3150-086-P1-N1-C1
Method	BLASTX
NCBI GI	g3024018
BLAST score	165
E value	5.0e-12
Match length	38
% identity	87
NCBI Description	INITIATION FACTOR 5A (EIF-5A) (EIF-4D) >gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation initiation factor 5A [Zea mays]
Seq. No.	298102
Seq. ID	LIB3150-086-P1-N1-D4
Method	BLASTN
NCBI GI	g168484
BLAST score	50
E value	1.0e-19
Match length	114
% identity	86
NCBI Description	Maize endosperm glutelin-2 gene, complete cds
Seq. No.	298103
Seq. ID	LIB3150-086-P1-N1-E8
Method	BLASTX

NCBI GI g1184776
BLAST score 293
E value 2.0e-26
Match length 63
% identity 90
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
GAPC4 [Zea mays]

Seq. No. 298104
Seq. ID LIB3150-087-P2-K1-C3
Method BLASTN
NCBI GI g498774
BLAST score 74
E value 9.0e-34
Match length 197
% identity 85
NCBI Description Z.mays (cv DH5xDH7) hsp70-5 mRNA for heat shock protein

Seq. No. 298105
Seq. ID LIB3150-087-P2-K1-D6
Method BLASTN
NCBI GI g927571
BLAST score 51
E value 2.0e-20
Match length 62
% identity 97
NCBI Description Z.mays mRNA for calreticulin precursor

Seq. No. 298106
Seq. ID LIB3150-087-P2-K1-E8
Method BLASTX
NCBI GI g861170
BLAST score 298
E value 5.0e-27
Match length 76
% identity 78
NCBI Description (X03697) heat shock protein 70 [Zea mays]

Seq. No. 298107
Seq. ID LIB3150-087-P2-K1-F1
Method BLASTN
NCBI GI g22516
BLAST score 114
E value 2.0e-57
Match length 198
% identity 89
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298108
Seq. ID LIB3150-087-P2-K1-F11
Method BLASTN
NCBI GI g2282583
BLAST score 38
E value 6.0e-12
Match length 134
% identity 83
NCBI Description Zea mays elongation factor 1-alpha (EF1-A) mRNA, complete

cds

Seq. No. 298109
Seq. ID LIB3150-087-P2-K1-G2
Method BLASTN
NCBI GI g22121
BLAST score 191
E value 1.0e-103
Match length 243
% identity 95
NCBI Description Maize alcohol dehydrogenase 1 gene (Adh1-1F)

Seq. No. 298110
Seq. ID LIB3150-088-P2-K1-A4
Method BLASTN
NCBI GI g22272
BLAST score 105
E value 7.0e-52
Match length 328
% identity 82
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)

Seq. No. 298111
Seq. ID LIB3150-088-P2-K1-B10
Method BLASTX
NCBI GI g3928086
BLAST score 157
E value 2.0e-10
Match length 45
% identity 58
NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

Seq. No. 298112
Seq. ID LIB3150-088-P2-K1-D11
Method BLASTX
NCBI GI g4586035
BLAST score 147
E value 3.0e-10
Match length 89
% identity 48
NCBI Description (AC007109) putative prohibitin protein [Arabidopsis thaliana]

Seq. No. 298113
Seq. ID LIB3150-088-P2-K1-F2
Method BLASTX
NCBI GI g4115937
BLAST score 226
E value 2.0e-18
Match length 51
% identity 75
NCBI Description (AF118223) contains similarity to human PCF11p homolog (GB:AF046935) [Arabidopsis thaliana]

Seq. No. 298114
Seq. ID LIB3150-089-P1-N1-B10
Method BLASTX

NCBI GI g417154
BLAST score 316
E value 2.0e-29
Match length 76
% identity 84
NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir_S25541 heat shock protein 82 - rice (strain Taichung Native One)
>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

Seq. No. 298115
Seq. ID LIB3150-089-P1-N1-B2
Method BLASTX
NCBI GI g417154
BLAST score 288
E value 5.0e-30
Match length 104
% identity 71
NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir_S25541 heat shock protein 82 - rice (strain Taichung Native One)
>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

Seq. No. 298116
Seq. ID LIB3150-089-P1-N1-F12
Method BLASTX
NCBI GI g2129626
BLAST score 360
E value 2.0e-34
Match length 88
% identity 76
NCBI Description J-domain protein - Arabidopsis thaliana
>gi_928936_emb_CAA89204_ (Z49238) J-domain protein [Arabidopsis thaliana] >gi_1585434_prf_2124427A diamide resistance gene [Arabidopsis thaliana]

Seq. No. 298117
Seq. ID LIB3150-089-P1-N1-G6
Method BLASTX
NCBI GI g3355475
BLAST score 177
E value 6.0e-13
Match length 81
% identity 53
NCBI Description (AC004218) ribosomal protein L23a [Arabidopsis thaliana]

Seq. No. 298118
Seq. ID LIB3150-089-P1-N1-H2
Method BLASTN
NCBI GI g2623247
BLAST score 51
E value 3.0e-20
Match length 107
% identity 88
NCBI Description Zea mays SU1 isoamylase (sugary1) gene, complete cds

Seq. No. 298119

Seq. ID LIB3150-089-P1-N1-H6
Method BLASTX
NCBI GI g1711036
BLAST score 264
E value 3.0e-23
Match length 95
% identity 63
NCBI Description (U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum sativum]

Seq. No. 298120
Seq. ID LIB3150-089-P2-K1-A5
Method BLASTN
NCBI GI g3318612
BLAST score 162
E value 6.0e-86
Match length 223
% identity 92
NCBI Description Zea mays mRNA for mitochondrial phosphate transporter, complete cds

Seq. No. 298121
Seq. ID LIB3150-089-P2-K1-B5
Method BLASTN
NCBI GI g342631
BLAST score 56
E value 9.0e-23
Match length 175
% identity 84
NCBI Description Maize mitochondrial F-1-ATPase subunit-2 mRNA, complete cds

Seq. No. 298122
Seq. ID LIB3150-089-P2-K1-G11
Method BLASTN
NCBI GI g168581
BLAST score 79
E value 2.0e-36
Match length 221
% identity 85
NCBI Description Z. mays pyruvate,orthophosphate dikinase (PPDK2) gene, 3' end

Seq. No. 298123
Seq. ID LIB3150-090-P2-K1-C11
Method BLASTN
NCBI GI g602252
BLAST score 89
E value 1.0e-42
Match length 141
% identity 91
NCBI Description Zea mays enolase (eno2) mRNA, complete cds

Seq. No. 298124
Seq. ID LIB3150-090-P2-K1-C3
Method BLASTN
NCBI GI g2642323
BLAST score 205

E value 1.0e-111
Match length 297
% identity 93
NCBI Description Zea mays profilin (PRO4) mRNA, complete cds

Seq. No. 298125
Seq. ID LIB3150-090-P2-K1-D4
Method BLASTX
NCBI GI g4490708
BLAST score 166
E value 2.0e-11
Match length 56
% identity 57
NCBI Description (AL035680) putative protein [Arabidopsis thaliana]

Seq. No. 298126
Seq. ID LIB3150-091-P1-N1-A4
Method BLASTX
NCBI GI g22166
BLAST score 212
E value 4.0e-23
Match length 89
% identity 71
NCBI Description (X15711) adenine nucleotide translocator [Zea mays]

Seq. No. 298127
Seq. ID LIB3150-091-P1-N1-A8
Method BLASTX
NCBI GI g451193
BLAST score 204
E value 4.0e-16
Match length 52
% identity 81
NCBI Description (L28008) wali7 [Triticum aestivum]
>gi_1090845_prf_2019486B wali7 gene [Triticum aestivum]

Seq. No. 298128
Seq. ID LIB3150-091-P1-N1-B10
Method BLASTN
NCBI GI g5091496
BLAST score 40
E value 3.0e-13
Match length 166
% identity 82
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence

Seq. No. 298129
Seq. ID LIB3150-091-P1-N1-D8
Method BLASTX
NCBI GI g3355620
BLAST score 165
E value 2.0e-11
Match length 40
% identity 85
NCBI Description (AJ000235) partial sequence, homology to phosphoribosylformylglycinamidine synthase [Hordeum

vulgaris]

Seq. No. 298130
Seq. ID LIB3150-091-P1-N1-F1
Method BLASTN
NCBI GI g2431768
BLAST score 64
E value 2.0e-27
Match length 160
% identity 85
NCBI Description Zea mays acidic ribosomal protein Pla (rpp1a) mRNA, complete cds

Seq. No. 298131
Seq. ID LIB3150-091-P1-N1-G4
Method BLASTX
NCBI GI g3236242
BLAST score 176
E value 8.0e-13
Match length 100
% identity 45
NCBI Description (AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No. 298132
Seq. ID LIB3150-091-P1-N1-G7
Method BLASTX
NCBI GI g1174613
BLAST score 162
E value 1.0e-14
Match length 84
% identity 57
NCBI Description 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) >gi_556560_dbj_BAA04614_ (D17788) rice homologue of Tat binding protein [Oryza sativa]

Seq. No. 298133
Seq. ID LIB3150-092-P1-N1-B1
Method BLASTX
NCBI GI g462243
BLAST score 208
E value 1.0e-16
Match length 85
% identity 61
NCBI Description HISTONE H4 >gi_421921_pir_S32769 histone H4 - tomato >gi_297150_emb_CAA48923_ (X69179) histone H4 [Lycopersicon esculentum] >gi_297152_emb_CAA48924_ (X69180) histone H4 [Lycopersicon esculentum] >gi_2746721 (AF038387) histone H4 [Capsicum annuum]

Seq. No. 298134
Seq. ID LIB3150-092-P1-N1-B4
Method BLASTX
NCBI GI g461498
BLAST score 227
E value 8.0e-19

Match length 92
 % identity 58
 NCBI Description ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2) (ALAAT-2) >gi_320619_pir_S28429 alanine transaminase (EC 2.6.1.2) - proso millet >gi_296204_emb_CAA49199_ (X69421) alanine aminotransferase [Panicum miliaceum]

Seq. No. 298135
 Seq. ID LIB3150-092-P1-N1-C3
 Method BLASTX
 NCBI GI g627584
 BLAST score 168
 E value 6.0e-12
 Match length 114
 % identity 34
 NCBI Description protein p84 - human >gi_550058 (L36529) protein p84 [Homo sapiens]

Seq. No. 298136
 Seq. ID LIB3150-092-P1-N1-D8
 Method BLASTX
 NCBI GI g1174867
 BLAST score 151
 E value 1.0e-11
 Match length 71
 % identity 58
 NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2 KD PROTEIN) >gi_633687_emb_CAA55862 (X79275) ubiquinol--cytochrome c reductase [Solanum tuberosum] >gi_1094912_prf_2107179A cytochrome c oxidase:SUBUNIT=8.2kD [Solanum tuberosum]

Seq. No. 298137
 Seq. ID LIB3150-092-P2-K1-A4
 Method BLASTN
 NCBI GI g168492
 BLAST score 35
 E value 3.0e-10
 Match length 39
 % identity 97
 NCBI Description Corn histone H3 (H3C3) gene, complete cds

Seq. No. 298138
 Seq. ID LIB3150-092-P2-K1-D12
 Method BLASTN
 NCBI GI g1321660
 BLAST score 47
 E value 2.0e-17
 Match length 71
 % identity 92
 NCBI Description Rice mRNA for ascorbate peroxidase, complete cds

Seq. No. 298139
 Seq. ID LIB3150-092-P2-K1-E1
 Method BLASTN

NCBI GI g747916
BLAST score 44
E value 1.0e-15
Match length 124
% identity 85
NCBI Description Z.mays CaM2 mRNA for calmodulin

Seq. No. 298140
Seq. ID LIB3150-093-P1-N1-A3
Method BLASTX
NCBI GI g3163946
BLAST score 179
E value 2.0e-13
Match length 50
% identity 70
NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica]

Seq. No. 298141
Seq. ID LIB3150-093-P1-N1-A7
Method BLASTX
NCBI GI g3024018
BLAST score 166
E value 1.0e-11
Match length 89
% identity 42
NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
>gi_1546919_emb_CAA69225_ (Y07920) translation initiation
factor 5A [Zea mays] >gi_2668738 (AF034943) translation
initiation factor 5A [Zea mays]

Seq. No. 298142
Seq. ID LIB3150-093-P1-N1-A8
Method BLASTX
NCBI GI g22224897
BLAST score 211
E value 3.0e-17
Match length 68
% identity 56
NCBI Description (U67132) DNA-binding protein PcMYB1 [Petroselinum crispum]

Seq. No. 298143
Seq. ID LIB3150-093-P1-N1-F1
Method BLASTX
NCBI GI g113622
BLAST score 268
E value 3.0e-41
Match length 106
% identity 92
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
>gi_68197_pir_ADRZY fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - rice >gi_20204_emb_CAA37290
(X53130) fructose-diphosphate aldolase (AA 1-358) [Oryza
sativa]

Seq. No. 298144
Seq. ID LIB3150-093-P1-N1-G2
Method BLASTN

NCBI GI g4151124
 BLAST score 58
 E value 4.0e-24
 Match length 78
 % identity 94
 NCBI Description Zea mays PDI-like protein mRNA, complete cds

Seq. No. 298145
 Seq. ID LIB3150-093-P1-N1-H2
 Method BLASTX
 NCBI GI g1085973
 BLAST score 191
 E value 6.0e-15
 Match length 62
 % identity 65
 NCBI Description isopentyl pyrophosphate isomerase - Clarkia breweri
 (fragment) >gi_572635_emb_CAA57947_ (X82627) isopentenyl
 pyrophosphate isomerase [Clarkia breweri]

Seq. No. 298146
 Seq. ID LIB3150-093-P1-N1-H4
 Method BLASTN
 NCBI GI g22144
 BLAST score 180
 E value 8.0e-97
 Match length 205
 % identity 96
 NCBI Description Maize anaerobically regulated gene for fructose
 bisphosphate aldolase (EC 4.1.2.13)

Seq. No. 298147
 Seq. ID LIB3150-093-P1-N1-H5
 Method BLASTX
 NCBI GI g461498
 BLAST score 297
 E value 3.0e-27
 Match length 78
 % identity 79
 NCBI Description ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
 TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
 (ALAAT-2) >gi_320619_pir_S28429 alanine transaminase (EC
 2.6.1.2) - proso millet >gi_296204_emb_CAA49199_ (X69421)
 alanine aminotransferase [Panicum miliaceum]

Seq. No. 298148
 Seq. ID LIB3150-093-P2-K1-C10
 Method BLASTN
 NCBI GI g1154858
 BLAST score 45
 E value 4.0e-16
 Match length 145
 % identity 82
 NCBI Description H.vulgare mRNA for L24 ribosomal protein

Seq. No. 298149
 Seq. ID LIB3150-093-P2-K1-F2
 Method BLASTX

NCBI GI g3885884
BLAST score 211
E value 6.0e-17
Match length 45
% identity 89
NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No. 298150
Seq. ID LIB3150-094-P1-N1-C5
Method BLASTN
NCBI GI g22272
BLAST score 41
E value 5.0e-14
Match length 65
% identity 91
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)

Seq. No. 298151
Seq. ID LIB3150-094-P1-N1-C8
Method BLASTX
NCBI GI g1351014
BLAST score 205
E value 3.0e-16
Match length 91
% identity 54
NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj_BAA07207_ (D38010)
ribosomal protein S8 [Oryza sativa]

Seq. No. 298152
Seq. ID LIB3150-094-P1-N1-D6
Method BLASTX
NCBI GI g4469020
BLAST score 180
E value 2.0e-13
Match length 66
% identity 48
NCBI Description (AL035602) putative protein (fragment) [Arabidopsis thaliana]

Seq. No. 298153
Seq. ID LIB3150-094-P1-N1-F2
Method BLASTX
NCBI GI g4115918
BLAST score 200
E value 1.0e-15
Match length 44
% identity 86
NCBI Description (AF118222) similar to nascent polypeptide associated complex alpha chain [Arabidopsis thaliana]

Seq. No. 298154
Seq. ID LIB3150-094-P1-N1-F8
Method BLASTX
NCBI GI g4539437
BLAST score 345
E value 1.0e-35
Match length 122

% identity 64
NCBI Description (AL049523) putative protein [Arabidopsis thaliana]

Seq. No. 298155
Seq. ID LIB3150-094-P1-N1-G12
Method BLASTX
NCBI GI g1332579
BLAST score 492
E value 9.0e-50
Match length 132
% identity 8
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 298156
Seq. ID LIB3150-094-P1-N1-G7
Method BLASTN
NCBI GI g2282583
BLAST score 38
E value 4.0e-12
Match length 106
% identity 84
NCBI Description Zea mays elongation factor 1-alpha (EF1-A) mRNA, complete cds

Seq. No. 298157
Seq. ID LIB3150-094-P2-K1-C12
Method BLASTX
NCBI GI g3128181
BLAST score 157
E value 2.0e-10
Match length 51
% identity 61
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 298158
Seq. ID LIB3150-094-P2-K1-C2
Method BLASTN
NCBI GI g22516
BLAST score 57
E value 1.0e-23
Match length 109
% identity 88
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298159
Seq. ID LIB3150-094-P2-K1-E11
Method BLASTN
NCBI GI g312180
BLAST score 73
E value 6.0e-33
Match length 125
% identity 90
NCBI Description Z.mays GapC4 gene

Seq. No. 298160
Seq. ID LIB3150-094-P2-K1-E12
Method BLASTX

NCBI GI g121296
BLAST score 362
E value 1.0e-34
Match length 109
% identity 60
NCBI Description 1,4-ALPHA-GLUCAN BRANCHING ENZYME (GLYCOGEN BRANCHING ENZYME) >gi_66573_pir_NQECA 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) - Escherichia coli >gi_146142 (M13751) branching enzyme (EC 2.4.1.18) [Escherichia coli]
>gi_1789839 (AE000419) 1,4-alpha-glucan branching enzyme [Escherichia coli]

Seq. No. 298161
Seq. ID LIB3150-094-P2-K1-G8
Method BLASTX
NCBI GI g2583123
BLAST score 226
E value 1.0e-18
Match length 47
% identity 83
NCBI Description (AC002387) putative nucleotide sugar epimerase [Arabidopsis thaliana]

Seq. No. 298162
Seq. ID LIB3150-095-P1-N1-A1
Method BLASTX
NCBI GI g3738257
BLAST score 168
E value 2.0e-12
Match length 46
% identity 78
NCBI Description (AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No. 298163
Seq. ID LIB3150-095-P1-N1-B5
Method BLASTX
NCBI GI g2851508
BLAST score 327
E value 2.0e-30
Match length 87
% identity 70
NCBI Description 60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to ribosomal protein L21 (gb_L38826). ESTs
gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana]

Seq. No. 298164
Seq. ID LIB3150-095-P1-N1-C2
Method BLASTX
NCBI GI g4432819
BLAST score 153
E value 1.0e-10
Match length 48
% identity 62
NCBI Description (AC006593) putative kinesin light chain [Arabidopsis

thaliana]

Seq. No. 298165
Seq. ID LIB3150-095-P1-N1-D1
Method BLASTX
NCBI GI g122085
BLAST score 455
E value 2.0e-45
Match length 109
% identity 85
NCBI Description HISTONE H3 >gi_81641_pir_S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir_S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir_S57626 histone H3 - maize >gi_20251_emb_CAA31969 (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970 (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays] >gi_168497 (M13379) histone H3 [Zea mays] >gi_168506 (M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111 (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811 (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >gi_225459_prf_1303352A histone H3 [Helicoverpa zea] >gi_225839_prf_1314298B histone H3 [Arabidopsis thaliana]

Seq. No. 298166
Seq. ID LIB3150-095-P1-N1-D3
Method BLASTN
NCBI GI g1421729
BLAST score 38
E value 6.0e-12
Match length 110
% identity 84
NCBI Description Zea mays T cytoplasm male sterility restorer factor 2 (rf2) mRNA, complete cds

Seq. No. 298167
Seq. ID LIB3150-095-P1-N1-E1
Method BLASTN
NCBI GI g1037129
BLAST score 296
E value 1.0e-166
Match length 400
% identity 94
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298168
Seq. ID LIB3150-095-P1-N1-E12
Method BLASTX
NCBI GI g419803
BLAST score 249
E value 1.0e-21
Match length 69
% identity 68
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 298169
Seq. ID LIB3150-095-P2-K1-A7
Method BLASTN
NCBI GI g1154858
BLAST score 45
E value 2.0e-16
Match length 57
% identity 95
NCBI Description H.vulgare mRNA for L24 ribosomal protein

Seq. No. 298170
Seq. ID LIB3150-095-P2-K1-H12
Method BLASTN
NCBI GI g2341060
BLAST score 270
E value 1.0e-150
Match length 314
% identity 96
NCBI Description Zea mays translational initiation factor eIF-4A (tif-4A3) mRNA, complete cds

Seq. No. 298171
Seq. ID LIB3150-096-P1-N1-D10
Method BLASTX
NCBI GI g99771
BLAST score 335
E value 2.0e-31
Match length 109
% identity 66
NCBI Description ubiquitin 81-aa extension protein 1 - Arabidopsis thaliana >gi_166934 (J05539) ubiquitin extension protein (UBQ5) [Arabidopsis thaliana]

Seq. No. 298172
Seq. ID LIB3150-096-P1-N1-D2
Method BLASTX
NCBI GI g22168
BLAST score 231
E value 9.0e-20
Match length 62
% identity 76
NCBI Description (X15712) adenine nucleotide translocator [Zea mays]

Seq. No. 298173
Seq. ID LIB3150-096-P1-N1-D3
Method BLASTX

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NCBI GI	g1136122
BLAST score	496
E value	2.0e-50
Match length	119
% identity	79
NCBI Description	(X91807) alfa-tubulin [Oryza sativa]
Seq. No.	298174
Seq. ID	LIB3150-096-P1-N1-E1
Method	BLASTX
NCBI GI	g3925363
BLAST score	157
E value	1.0e-10
Match length	94
% identity	46
NCBI Description	(AF067961) homeodomain protein [Malus domestica]
Seq. No.	298175
Seq. ID	LIB3150-096-P1-N1-E7
Method	BLASTX
NCBI GI	g1723669
BLAST score	153
E value	5.0e-10
Match length	78
% identity	41
NCBI Description	HYPOTHETICAL 71.3 KD PROTEIN IN SCM4-MUP1 INTERGENIC REGION >gi_2131657_pir_S64348 hypothetical protein YGR054w - yeast (Saccharomyces cerevisiae) >gi_1323065_emb_CAA97054_(Z72839) ORF YGR054w [Saccharomyces cerevisiae]
Seq. No.	298176
Seq. ID	LIB3150-096-P1-N1-G4
Method	BLASTX
NCBI GI	g2505940
BLAST score	172
E value	2.0e-12
Match length	65
% identity	58
NCBI Description	(Y13071) 26S proteasome, non-ATPase subunit [Mus musculus]
Seq. No.	298177
Seq. ID	LIB3150-097-P1-N1-A8
Method	BLASTX
NCBI GI	g312179
BLAST score	386
E value	2.0e-37
Match length	86
% identity	87
NCBI Description	(X73151) glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays] >gi_1185554 (U45858) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
Seq. No.	298178
Seq. ID	LIB3150-097-P1-N1-E7
Method	BLASTN

NCBI GI 922292
BLAST score 50
E value 4.0e-19
Match length 82
% identity 91
NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 298179
Seq. ID LIB3150-097-P1-N1-E9
Method BLASTX
NCBI GI g2129946
BLAST score 346
E value 1.0e-32
Match length 87
% identity 80
NCBI Description ADP-ribosylation factor homolog GTP-binding protein NTGB1 - common tobacco (fragment) >gi_1184987 (U46927) NTGB1 [Nicotiana tabacum]

Seq. No. 298180
Seq. ID LIB3150-097-P1-N1-F7
Method BLASTX
NCBI GI g1703374
BLAST score 199
E value 2.0e-15
Match length 72
% identity 67
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_2129457_pir_S66337
ADP-ribosylation factor 1 - Chlamydomonas reinhardtii
>gi_861205 (U27120) ADP-ribosylation factor [Chlamydomonas reinhardtii]

Seq. No. 298181
Seq. ID LIB3150-097-P1-N1-F9
Method BLASTX
NCBI GI g1184774
BLAST score 232
E value 2.0e-26
Match length 103
% identity 69
NCBI Description (U45856) cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]

Seq. No. 298182
Seq. ID LIB3150-097-P1-N1-G7
Method BLASTX
NCBI GI g1184774
BLAST score 204
E value 8.0e-25
Match length 95
% identity 72
NCBI Description (U45856) cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]

Seq. No. 298183
Seq. ID LIB3150-097-P1-N1-H10
Method BLASTN

NCBI GI g571474
BLAST score 33
E value 4.0e-09
Match length 65
% identity 88
NCBI Description Chlamydomonas reinhardtii histone H3 (ch3-III), histone H4 (ch4-III), histone H2B (ch2b-III) and histone H2A (ch2a-III) genes, complete cds

Seq. No. 298184
Seq. ID LIB3150-098-P1-N1-B1
Method BLASTX
NCBI GI g1658313
BLAST score 210
E value 6.0e-17
Match length 52
% identity 75
NCBI Description (Y08987) osr40g2 [Oryza sativa]

Seq. No. 298185
Seq. ID LIB3150-098-P1-N1-B9
Method BLASTX
NCBI GI g3176711
BLAST score 192
E value 1.0e-14
Match length 88
% identity 57
NCBI Description (AC002392) bZIP-like protein [Arabidopsis thaliana]

Seq. No. 298186
Seq. ID LIB3150-098-P1-N1-D3
Method BLASTX
NCBI GI g4469005
BLAST score 242
E value 2.0e-20
Match length 88
% identity 51
NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No. 298187
Seq. ID LIB3150-098-P1-N1-E5
Method BLASTX
NCBI GI g3015621
BLAST score 236
E value 3.0e-20
Match length 72
% identity 72
NCBI Description (AF035460) low molecular weight heat shock protein precursor [Zea mays]

Seq. No. 298188
Seq. ID LIB3150-098-P1-N1-H4
Method BLASTX
NCBI GI g2499932
BLAST score 172
E value 1.0e-12
Match length 52

% identity 67
NCBI Description ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi_726305
(U22442) adenine phosphoribosyltransferase form 1 [Triticum
aestivum]

Seq. No. 298189
Seq. ID LIB3150-099-P1-N1-F12
Method BLASTX
NCBI GI g3687251
BLAST score 208
E value 8.0e-17
Match length 62
% identity 63
NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]

Seq. No. 298190
Seq. ID LIB3150-099-P1-N1-H8
Method BLASTN
NCBI GI g22172
BLAST score 39
E value 1.0e-12
Match length 71
% identity 89
NCBI Description Maize ATP2 mRNA for mitochondrial ATP synthase beta subunit

Seq. No. 298191
Seq. ID LIB3150-100-P1-N1-A7
Method BLASTN
NCBI GI g2811133
BLAST score 125
E value 4.0e-64
Match length 201
% identity 91
NCBI Description Zea mays starch synthase isoform zSTSII-1 (zSSIIa) mRNA,
partial cds

Seq. No. 298192
Seq. ID LIB3150-100-P1-N1-E1
Method BLASTX
NCBI GI g4530611
BLAST score 401
E value 4.0e-39
Match length 81
% identity 91
NCBI Description (AF134552) serine/threonine protein phosphatase PP2A-2
catalytic subunit [Oryza sativa subsp. indica]

Seq. No. 298193
Seq. ID LIB3150-100-P1-N1-E12
Method BLASTX
NCBI GI g2244760
BLAST score 155
E value 9.0e-11
Match length 62
% identity 50
NCBI Description (Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No. 298194
Seq. ID LIB3150-100-P1-N1-H3
Method BLASTN
NCBI GI g1037129
BLAST score 284
E value 1.0e-159
Match length 358
% identity 95
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298195
Seq. ID LIB3150-100-P1-N1-H5
Method BLASTX
NCBI GI g1168609
BLAST score 188
E value 2.0e-14
Match length 71
% identity 51
NCBI Description AUXIN-RESISTANCE PROTEIN AXR1 >gi_479664_pir_S35071 auxin-resistance protein AXR1 - Arabidopsis thaliana >gi_304104 (L13922) ubiquitin-activating enzyme E1 [Arabidopsis thaliana] >gi_2388579 (AC000098) Match to Arabidopsis AXR1 (gb_ATHAXR1122). [Arabidopsis thaliana] >gi_448755_prf_1917337A ubiquitin-activating enzyme E1 [Arabidopsis thaliana]

Seq. No. 298196
Seq. ID LIB3150-100-P2-K1-C5
Method BLASTX
NCBI GI g445612
BLAST score 149
E value 2.0e-09
Match length 39
% identity 77
NCBI Description ribosomal protein S19 [Solanum tuberosum]

Seq. No. 298197
Seq. ID LIB3150-100-P2-K1-D1
Method BLASTX
NCBI GI g1351270
BLAST score 238
E value 5.0e-20
Match length 53
% identity 89
NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_478410_pir_JQ2255 triose-phosphate isomerase (EC 5.3.1.1) - rice >gi_169821 (M87064) triosephosphate isomerase [Oryza sativa]

Seq. No. 298198
Seq. ID LIB3150-100-P2-K1-D8
Method BLASTN
NCBI GI g22469
BLAST score 61
E value 9.0e-26
Match length 207

% identity 81
NCBI Description Maize mRNA for cytoplasmic ribosomal protein S11

Seq. No. 298199
Seq. ID LIB3150-100-P2-K1-E6
Method BLASTX
NCBI GI g3372518
BLAST score 635
E value 1.0e-66
Match length 123
% identity 97
NCBI Description (AF050631) invertase [Zea mays]

Seq. No. 298200
Seq. ID LIB3150-101-P1-N1-C3
Method BLASTX
NCBI GI g1711036
BLAST score 322
E value 5.0e-30
Match length 98
% identity 66
NCBI Description (U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum sativum]

Seq. No. 298201
Seq. ID LIB3150-101-P1-N1-F11
Method BLASTX
NCBI GI g1184774
BLAST score 401
E value 3.0e-39
Match length 91
% identity 85
NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]

Seq. No. 298202
Seq. ID LIB3150-102-P2-K1-E7
Method BLASTN
NCBI GI g2340107
BLAST score 95
E value 4.0e-46
Match length 186
% identity 89
NCBI Description Zea mays starch branching enzyme IIa (Sbe2a) mRNA, partial cds

Seq. No. 298203
Seq. ID LIB3150-103-P2-K1-A11
Method BLASTX
NCBI GI g136063
BLAST score 157
E value 2.0e-10
Match length 35
% identity 91
NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
>gi_68426_pir_ISZMT triose-phosphate isomerase (EC
5.3.1.1) - maize >gi_168647 (L00371) triosephosphate

isomerase 1 [Zea mays] >gi_217974_dbj_BAA00009_ (D00012)
triosephosphaté isomerase [Zea mays]

Seq. No. 298204
Seq. ID LIB3150-103-P2-K1-B11
Method BLASTX
NCBI GI g1076531
BLAST score 166
E value 2.0e-11
Match length 38
% identity 82
NCBI Description hypothetical protein, pollen allergen homolog - garden pea
>gi_2129891_pir_S65056 pollen allergen homolog precursor
(clone PPA1) - garden pea >gi_732905_emb_CAA59470_ (X85187)
homology with pollen allergens [Pisum sativum]

Seq. No. 298205
Seq. ID LIB3150-103-P2-K1-D3
Method BLASTX
NCBI GI g4150963
BLAST score 164
E value 3.0e-11
Match length 57
% identity 60
NCBI Description (Y18620) DsPTP1 protein [Arabidopsis thaliana]

Seq. No. 298206
Seq. ID LIB3150-103-P2-K1-E8
Method BLASTN
NCBI GI g625147
BLAST score 144
E value 3.0e-75
Match length 270
% identity 97
NCBI Description Zea mays protein disulfide isomerase (pdi) mRNA, complete
cds

Seq. No. 298207
Seq. ID LIB3150-103-P2-K1-F7
Method BLASTX
NCBI GI g1076820
BLAST score 166
E value 1.0e-11
Match length 41
% identity 80
NCBI Description phosphoglycerate mutase (EC 5.4.2.1) - maize

Seq. No. 298208
Seq. ID LIB3150-103-P2-K1-G12
Method BLASTX
NCBI GI g731827
BLAST score 143
E value 9.0e-09
Match length 54
% identity 50
NCBI Description MITOCHONDRIAL ACIDIC PROTEIN MAM33 PRECURSOR
>gi_626327_pir_S48409 hypothetical protein YIL070c - yeast

(*Saccharomyces cerevisiae*) >gi_557799_emb_CAA86153_
(Z38060) orf, len: 266, CAI: 0.21 [*Saccharomyces*
cerevisiae]

Seq. No. 298209
Seq. ID LIB3150-104-P2-K1-A5
Method BLASTX
NCBI GI g1762945
BLAST score 150
E value 1.0e-09
Match length 45
% identity 69
NCBI Description (U66269) ORF; able to induce HR-like lesions [*Nicotiana tabacum*]

Seq. No. 298210
Seq. ID LIB3150-104-P2-K1-D5
Method BLASTX
NCBI GI g3790441
BLAST score 148
E value 2.0e-09
Match length 36
% identity 89
NCBI Description (AF030515) chaperonin 60 alpha subunit [*Canavalia lineata*]

Seq. No. 298211
Seq. ID LIB3150-104-P2-K1-D8
Method BLASTN
NCBI GI g2662309
BLAST score 41
E value 8.0e-14
Match length 61
% identity 92
NCBI Description *Hordeum vulgare* mRNA for bpwl, complete cds

Seq. No. 298212
Seq. ID LIB3150-104-P2-K1-F1
Method BLASTX
NCBI GI g3334323
BLAST score 374
E value 7.0e-36
Match length 87
% identity 83
NCBI Description GTP-BINDING PROTEIN SAR1A >gi_1314860 (U56929) Sar1 homolog [*Arabidopsis thaliana*] >gi_2104532_gb_AAC78700.1 (AF001308) SAR1/GTP-binding secretory factor [*Arabidopsis thaliana*] >gi_2104550 (AF001535) AGAA.4 [*Arabidopsis thaliana*]

Seq. No. 298213
Seq. ID LIB3150-104-P2-K1-F2
Method BLASTN
NCBI GI g3925236
BLAST score 74
E value 2.0e-33
Match length 152
% identity 87

NCBI Description Zea mays 6-phosphogluconate dehydrogenase gene, partial cds

Seq. No. 298214

Seq. ID LIB3150-104-P2-K1-H6

Method BLASTX

NCBI GI g3763917

BLAST score 209

E value 8.0e-17

Match length 44

% identity 84

NCBI Description (AC004450) hypothetical protein [Arabidopsis thaliana]
>gi_4531438_gb_AAD22123.1 AC006224_5 (AC006224)
hypothetical protein [Arabidopsis thaliana]

Seq. No. 298215

Seq. ID LIB3150-105-P2-K1-A4

Method BLASTN

NCBI GI g902526

BLAST score 84

E value 1.0e-39

Match length 136

% identity 90

NCBI Description Zea mays clone MubG7 ubiquitin fusion protein gene,
complete cds

Seq. No. 298216

Seq. ID LIB3150-105-P2-K1-B7

Method BLASTN

NCBI GI g2642323

BLAST score 246

E value 1.0e-136

Match length 279

% identity 97

NCBI Description Zea mays profilin (PRO4) mRNA, complete cds

Seq. No. 298217

Seq. ID LIB3150-105-P2-K1-E5

Method BLASTN

NCBI GI g217973

BLAST score 131

E value 1.0e-67

Match length 230

% identity 92

NCBI Description Zea mays gene for triosephosphate isomerase, complete cds

Seq. No. 298218

Seq. ID LIB3150-105-P2-K1-G1

Method BLASTN

NCBI GI g602252

BLAST score 42

E value 1.0e-14

Match length 211

% identity 78

NCBI Description Zea mays enolase (eno2) mRNA, complete cds

Seq. No. 298219

Seq. ID LIB3150-106-P2-K1-B5

Method BLASTX
NCBI GI g2230873
BLAST score 197
E value 4.0e-15
Match length 67
% identity 60
NCBI Description (X98494) M phase phosphoprotein 10 [Homo sapiens]

Seq. No. 298220
Seq. ID LIB3150-106-P2-K1-F12
Method BLASTN
NCBI GI g1335965
BLAST score 40
E value 3.0e-13
Match length 148
% identity 82
NCBI Description Zea mays acetyl CoA carboxylase mRNA, partial cds

Seq. No. 298221
Seq. ID LIB3150-106-P2-K1-F3
Method BLASTX
NCBI GI g1172977
BLAST score 359
E value 3.0e-34
Match length 77
% identity 86
NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No. 298222
Seq. ID LIB3150-106-P2-K1-H1
Method BLASTX
NCBI GI g1076800
BLAST score 215
E value 3.0e-17
Match length 57
% identity 77
NCBI Description L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme - maize >gi_600116_emb_CAA84406 (Z34934) cytosolic ascorbate peroxidase [Zea mays] >gi_1096503_prf_2111423A ascorbate peroxidase [Zea mays]

Seq. No. 298223
Seq. ID LIB3150-106-P2-K1-H3
Method BLASTN
NCBI GI g22144
BLAST score 292
E value 1.0e-163
Match length 344
% identity 96
NCBI Description Maize anaerobically regulated gene for fructose bisphosphate aldolase (EC 4.1.2.13)

Seq. No. 298224
Seq. ID LIB3150-106-P2-K1-H8
Method BLASTX
NCBI GI g2996166

09580112-1000

BLAST score 255
E value 5.0e-22
Match length 55
% identity 82
NCBI Description (AF051757) putative 60S ribosomal protein L15 [Picea mariana] >gi_2996168 (AF051758) putative 60S ribosomal protein L15 [Picea mariana] >gi_2996170 (AF051759) putative 60S ribosomal protein L15 [Picea mariana]

Seq. No. 298225
Seq. ID LIB3150-107-P1-N1-E12
Method BLASTX
NCBI GI g3548818
BLAST score 206
E value 3.0e-16
Match length 113
% identity 43
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]

Seq. No. 298226
Seq. ID LIB3150-107-P1-N1-E4
Method BLASTN
NCBI GI g577818
BLAST score 62
E value 2.0e-26
Match length 125
% identity 89
NCBI Description Z.mays gene for H2B histone (gH2B4)

Seq. No. 298227
Seq. ID LIB3150-107-P1-N1-F4
Method BLASTX
NCBI GI g462195
BLAST score 242
E value 2.0e-20
Match length 71
% identity 66
NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
>gi_100682_pir_S21636 GOS2 protein - rice
>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
>gi_3789950_ (AF094774) translation initiation factor [Oryza sativa]

Seq. No. 298228
Seq. ID LIB3150-107-P1-N1-H4
Method BLASTX
NCBI GI g4510423
BLAST score 175
E value 7.0e-13
Match length 87
% identity 45
NCBI Description (AC006929) unknown protein [Arabidopsis thaliana]

Seq. No. 298229
Seq. ID LIB3150-107-P2-K1-A10
Method BLASTN
NCBI GI g498774

BLAST score 220
E value 1.0e-120
Match length 267
% identity 96
NCBI Description Z.mays (cv DH5xDH7) hsp70-5 mRNA for heat shock protein

Seq. No. 298230
Seq. ID LIB3150-107-P2-K1-B10
Method BLASTX
NCBI GI g2492519
BLAST score 161
E value 6.0e-11
Match length 43
% identity 77
NCBI Description 26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase subunit [Spinacia oleracea]

Seq. No. 298231
Seq. ID LIB3150-107-P2-K1-B5
Method BLASTN
NCBI GI g498772
BLAST score 143
E value 1.0e-74
Match length 252
% identity 89
NCBI Description Z.mays (cv DH5xDH7) hsp70-4 mRNA for heat shock protein

Seq. No. 298232
Seq. ID LIB3150-107-P2-K1-F12
Method BLASTN
NCBI GI g2341060
BLAST score 181
E value 3.0e-97
Match length 285
% identity 91
NCBI Description Zea mays translational initiation factor eIF-4A (tif-4A3) mRNA, complete cds

Seq. No. 298233
Seq. ID LIB3150-107-P2-K1-H2
Method BLASTN
NCBI GI g22324
BLAST score 172
E value 6.0e-92
Match length 212
% identity 95
NCBI Description Z.mays mRNA for H2B histone (clone cH2B221)

Seq. No. 298234
Seq. ID LIB3150-108-P1-N1-A11
Method BLASTX
NCBI GI g1658313
BLAST score 148
E value 2.0e-09
Match length 102
% identity 39

09569046 * 46010000

NCBI Description (Y08987) osr40g2 [Oryza sativa]
Seq. No. 298235
Seq. ID LIB3150-108-P1-N1-C4
Method BLASTX
NCBI GI g419803
BLAST score 347
E value 1.0e-32
Match length 122
% identity 60
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 298236
Seq. ID LIB3150-108-P1-N1-C5
Method BLASTX
NCBI GI g168664
BLAST score 317
E value 2.0e-29
Match length 65
% identity 88
NCBI Description (M13507) zein protein precursor [Zea mays]

Seq. No. 298237
Seq. ID LIB3150-108-P1-N1-E2
Method BLASTX
NCBI GI g3335372
BLAST score 172
E value 3.0e-12
Match length 122
% identity 38
NCBI Description (AC003028) putative SRG1 protein [Arabidopsis thaliana]

Seq. No. 298238
Seq. ID LIB3150-108-P1-N1-E5
Method BLASTX
NCBI GI g1658313
BLAST score 321
E value 8.0e-30
Match length 91
% identity 34
NCBI Description (Y08987) osr40g2 [Oryza sativa]

Seq. No. 298239
Seq. ID LIB3150-108-P1-N1-G2
Method BLASTX
NCBI GI g3746936
BLAST score 175
E value 3.0e-13
Match length 69
% identity 54
NCBI Description (AF091808) actin 1 [Anemia phyllitidis]

Seq. No. 298240
Seq. ID LIB3150-108-P1-N1-H7
Method BLASTX
NCBI GI g2282584

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BLAST score 486
E value 4.0e-49
Match length 110
% identity 85
NCBI Description (U76259) elongation factor 1-alpha [Zea mays]

Seq. No. 298241
Seq. ID LIB3150-108-P2-K1-B9
Method BLASTN
NCBI GI g1575127
BLAST score 103
E value 1.0e-50
Match length 345
% identity 82
NCBI Description Zea mays luminal binding protein cBiPe2 mRNA, complete cds

Seq. No. 298242
Seq. ID LIB3150-108-P2-K1-E10
Method BLASTX
NCBI GI g4445613
BLAST score 174
E value 2.0e-12
Match length 50
% identity 64
NCBI Description ribosomal protein L7 [Solanum tuberosum]

Seq. No. 298243
Seq. ID LIB3150-108-P2-K1-E5
Method BLASTN
NCBI GI g168512
BLAST score 147
E value 6.0e-77
Match length 365
% identity 88
NCBI Description Maize major protein (L3) mRNA from the surface of lipid bodies, 3' end

Seq. No. 298244
Seq. ID LIB3150-108-P2-K1-F7
Method BLASTX
NCBI GI g4512699
BLAST score 181
E value 3.0e-13
Match length 53
% identity 62
NCBI Description (AC006569) putative NADH-ubiquinone oxireductase [Arabidopsis thaliana]

Seq. No. 298245
Seq. ID LIB3150-108-P2-K1-H3
Method BLASTN
NCBI GI g1184773
BLAST score 154
E value 3.0e-81
Match length 182
% identity 97
NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC3

(gpc3) mRNA, complete cds

Seq. No. 298246
Seq. ID LIB3150-109-P2-K1-A4
Method BLASTX
NCBI GI g2827700
BLAST score 200
E value 2.0e-15
Match length 84
% identity 49
NCBI Description (AL021684) DEAD box ATP dependent helicase protein [Arabidopsis thaliana]

Seq. No. 298247
Seq. ID LIB3150-109-P2-K1-B5
Method BLASTX
NCBI GI g4309698
BLAST score 307
E value 4.0e-28
Match length 130
% identity 56
NCBI Description (AC006266) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No. 298248
Seq. ID LIB3150-109-P2-K1-D12
Method BLASTN
NCBI GI g22272
BLAST score 98
E value 1.0e-47
Match length 287
% identity 86
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)

Seq. No. 298249
Seq. ID LIB3150-109-P2-K1-E6
Method BLASTN
NCBI GI g168505
BLAST score 41
E value 5.0e-14
Match length 45
% identity 98
NCBI Description Zea mays histone H3 gene, complete cds

Seq. No. 298250
Seq. ID LIB3150-109-P2-K1-F10
Method BLASTX
NCBI GI g1169533
BLAST score 335
E value 3.0e-31
Match length 81
% identity 85
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
>gi_515827_emb_CAA56645_ (X80474) enolase [Neocallimastix frontalis]

DRAFT 02/20/2000

Seq. No. 298251
Seq. ID LIB3150-109-P2-K1-G2
Method BLASTX
NCBI GI g136057
BLAST score 194
E value 9.0e-15
Match length 45
% identity 84
NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
>gi_99499_pir_A32187 (S)-tetrahydroberberine oxidase -
Coptis japonica >gi_556171 (J04121) triosephosphate
isomerase [Coptis japonica]

Seq. No. 298252
Seq. ID LIB3150-109-P2-K1-H10
Method BLASTN
NCBI GI g998429
BLAST score 144
E value 3.0e-75
Match length 333
% identity 85
NCBI Description GRF1=general regulatory factor [Zea mays, XL80, Genomic,
5348 nt]

Seq. No. 298253
Seq. ID LIB3150-110-P2-K1-C4
Method BLASTN
NCBI GI g22272
BLAST score 72
E value 3.0e-32
Match length 215
% identity 82
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)

Seq. No. 298254
Seq. ID LIB3150-110-P2-K1-D11
Method BLASTN
NCBI GI g1532072
BLAST score 72
E value 4.0e-32
Match length 247
% identity 81
NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase

Seq. No. 298255
Seq. ID LIB3150-110-P2-K1-D12
Method BLASTN
NCBI GI g312178
BLAST score 89
E value 2.0e-42
Match length 143
% identity 58
NCBI Description Z.mays GapC2 gene

Seq. No. 298256
Seq. ID LIB3150-110-P2-K1-G2
Method BLASTN

NCBI GI g531832
BLAST score 36
E value 3.0e-11
Match length 76
% identity 87
NCBI Description Cloning vector pSport2, complete sequence

Seq. No. 298257
Seq. ID LIB3150-110-P2-K1-G6
Method BLASTN
NCBI GI g902585
BLAST score 35
E value 4.0e-10
Match length 55
% identity 91
NCBI Description Zea mays clone MubG9 ubiquitin gene, complete cds

Seq. No. 298258
Seq. ID LIB3150-111-P2-K1-C5
Method BLASTN
NCBI GI g293886
BLAST score 38
E value 6.0e-12
Match length 74
% identity 88
NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase mRNA, 3' end, (clone GACP3)

Seq. No. 298259
Seq. ID LIB3150-112-P2-K1-A3
Method BLASTX
NCBI GI g2695941
BLAST score 200
E value 1.0e-15
Match length 50
% identity 76
NCBI Description (AJ222784) ribosomal like-protein [Hordeum vulgare]

Seq. No. 298260
Seq. ID LIB3150-112-P2-K1-A5
Method BLASTX
NCBI GI g2498077
BLAST score 510
E value 8.0e-52
Match length 99
% identity 97
NCBI Description NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I) (PP18) >gi_1777930 (U55019) nucleoside diphosphate kinase [Saccharum officinarum]

Seq. No. 298261
Seq. ID LIB3150-112-P2-K1-A6
Method BLASTN
NCBI GI g2431766
BLAST score 173
E value 1.0e-92
Match length 217

% identity 95
NCBI Description Zea mays acidic ribosomal protein P3a (rpp3a) mRNA, complete cds

Seq. No. 298262
Seq. ID LIB3150-112-P2-K1-B7
Method BLASTX
NCBI GI g3860277
BLAST score 392
E value 5.0e-38
Match length 88
% identity 86
NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604 (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 298263
Seq. ID LIB3150-112-P2-K1-C2
Method BLASTX
NCBI GI g19614
BLAST score 171
E value 4.0e-12
Match length 45
% identity 78
NCBI Description (X13677) histone H3 (AA 1-58) [Medicago sativa]

Seq. No. 298264
Seq. ID LIB3150-112-P2-K1-F5
Method BLASTN
NCBI GI g1184773
BLAST score 44
E value 9.0e-16
Match length 116
% identity 86
NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase GACP3 (gpc3) mRNA, complete cds

Seq. No. 298265
Seq. ID LIB3150-112-P2-K1-G3
Method BLASTX
NCBI GI g1653293
BLAST score 160
E value 8.0e-11
Match length 58
% identity 57
NCBI Description (D90912) ornithine acetyltransferase [Synechocystis sp.]

Seq. No. 298266
Seq. ID LIB3150-112-P2-K1-H5
Method BLASTN
NCBI GI g2257755
BLAST score 202
E value 1.0e-110
Match length 311
% identity 91
NCBI Description Zea mays nucleolar histone deacetylase HD2-p39 mRNA, complete cds

Seq. No. 298267
Seq. ID LIB3150-113-P2-K1-C5
Method BLASTN
NCBI GI g2345153
BLAST score 175
E value 8.0e-94
Match length 255
% identity 93
NCBI Description Zea mays ribosomal protein S4 (rps4) mRNA, complete cds

Seq. No. 298268
Seq. ID LIB3150-113-P2-K1-C6
Method BLASTN
NCBI GI g3294466
BLAST score 43
E value 4.0e-15
Match length 127
% identity 82
NCBI Description Zea mays phosphoglucomutase 1 mRNA, complete cds

Seq. No. 298269
Seq. ID LIB3150-113-P2-K1-G5
Method BLASTN
NCBI GI g22516
BLAST score 160
E value 6.0e-85
Match length 212
% identity 94
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298270
Seq. ID LIB3150-113-P2-K1-H8
Method BLASTX
NCBI GI g4581156
BLAST score 290
E value 5.0e-26
Match length 63
% identity 90
NCBI Description (AC006919) putative pyruvate kinase [Arabidopsis thaliana]

Seq. No. 298271
Seq. ID LIB3150-114-P2-K1-C8
Method BLASTX
NCBI GI g1174536
BLAST score 144
E value 5.0e-09
Match length 37
% identity 70
NCBI Description ASPARAGINYL-TRNA SYNTHETASE (ASPARAGINE--TRNA LIGASE)
(ASNRS) >gi_1073865_pir_B64115 asparagine--tRNA ligase (EC
6.1.1.22) - *Haemophilus influenzae* (strain Rd KW20)
>gi_1574761 (U32810) asparaginyl-tRNA synthetase (asnS)
[*Haemophilus influenzae* Rd]

Seq. No. 298272
Seq. ID LIB3150-114-P2-K1-H5

Method BLASTN
NCBI GI g168694
BLAST score 59
E value 1.0e-24
Match length 125
% identity 94
NCBI Description Maize gamma zein mRNA, partial cds

Seq. No. 298273
Seq. ID LIB3150-116-P2-K1-B8
Method BLASTX
NCBI GI g1706323
BLAST score 217
E value 2.0e-17
Match length 114
% identity 45
NCBI Description ORNITHINE DECARBOXYLASE (ODC) >gi_2118242_pir_S64704
ornithine decarboxylase (EC 4.1.1.17) - jimsonweed
>gi_871008_emb_CAA61121_ (X87847) ornithine decarboxylase
[Datura stramonium]

Seq. No. 298274
Seq. ID LIB3150-116-P2-K1-G5
Method BLASTN
NCBI GI g1895083
BLAST score 34
E value 1.0e-09
Match length 86
% identity 85
NCBI Description Zea mays golgi associated protein se-wap41 mRNA, complete
cds

Seq. No. 298275
Seq. ID LIB3150-117-P2-K1-B7
Method BLASTX
NCBI GI g2642446
BLAST score 154
E value 3.0e-10
Match length 51
% identity 65
NCBI Description (AC002391) similar to auxin-responsive GH3 protein
[Arabidopsis thaliana]

Seq. No. 298276
Seq. ID LIB3150-117-P2-K1-F8
Method BLASTN
NCBI GI g2104711
BLAST score 41
E value 6.0e-14
Match length 69
% identity 90
NCBI Description Zea mays endosperm specific protein mRNA, complete cds

Seq. No. 298277
Seq. ID LIB3150-117-P2-K1-G4
Method BLASTN
NCBI GI g998429

BLAST score 211
 E value 1.0e-115
 Match length 319
 % identity 91
 NCBI Description GRF1=general regulatory factor [Zea mays, XL80, Genomic, 5348 nt]

Seq. No. 298278
 Seq. ID LIB3150-117-P2-K1-H6
 Method BLASTX
 NCBI GI g4506635
 BLAST score 186
 E value 5.0e-14
 Match length 61
 % identity 62
 NCBI Description ribosomal protein L32 >gi_132886_sp_P02433_RL32_HUMAN 60S RIBOSOMAL PROTEIN L32 >gi_71335_pir_R5HU32 ribosomal protein L32 - human >gi_71336_pir_R5MS32 ribosomal protein L32 - mouse >gi_71337_pir_R5RT32 ribosomal protein L32 - rat >gi_36132_emb_CAA27048 (X03342) rpL32 (aa 1-135) [Homo sapiens] >gi_57117_emb_CAA29777 (X06483) ribosomal protein L32 [Rattus norvegicus] >gi_200781 (K02060) ribosomal protein L32-3A [Mus musculus] >gi_226004_prf_1405339A ribosomal protein L32 [Rattus norvegicus]

Seq. No. 298279
 Seq. ID LIB3150-118-P2-K1-G9
 Method BLASTN
 NCBI GI g2431770
 BLAST score 60
 E value 5.0e-25
 Match length 228
 % identity 82
 NCBI Description Zea mays acidic ribosomal protein P2b (rpp2b) mRNA, complete cds

Seq. No. 298280
 Seq. ID LIB3151-001-P1-K1-A11
 Method BLASTX
 NCBI GI g22216
 BLAST score 246
 E value 4.0e-21
 Match length 64
 % identity 80
 NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 298281
 Seq. ID LIB3151-001-P1-K1-A4
 Method BLASTX
 NCBI GI g121472
 BLAST score 144
 E value 3.0e-12
 Match length 88
 % identity 50
 NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2) >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -

maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
 [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
 mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298282
 Seq. ID LIB3151-001-P1-K1-A8
 Method BLASTX
 NCBI GI g141597
 BLAST score 346
 E value 1.0e-32
 Match length 129
 % identity 63
 NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
 >gi_72314_pir_ZIZM3_19K zein precursor (clone A30) - maize
 >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
 [Zea mays]

Seq. No. 298283
 Seq. ID LIB3151-001-P1-K1-B6
 Method BLASTX
 NCBI GI g168701
 BLAST score 520
 E value 8.0e-55
 Match length 140
 % identity 79
 NCBI Description (M60837) zein [Zea mays]

Seq. No. 298284
 Seq. ID LIB3151-001-P1-K1-B7
 Method BLASTN
 NCBI GI g22549
 BLAST score 227
 E value 1.0e-125
 Match length 311
 % identity 93
 NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 298285
 Seq. ID LIB3151-001-P1-K1-C12
 Method BLASTX
 NCBI GI g141608
 BLAST score 160
 E value 2.0e-11
 Match length 64
 % identity 62
 NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
 zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
 zein [Zea mays]

Seq. No. 298286
 Seq. ID LIB3151-001-P1-K1-C5
 Method BLASTX
 NCBI GI g141597
 BLAST score 311
 E value 2.0e-28
 Match length 116
 % identity 60

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
 >gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
 >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
 [Zea mays]

Seq. No. 298287
 Seq. ID LIB3151-001-P1-K1-D10
 Method BLASTX
 NCBI GI g141617
 BLAST score 243
 E value 2.0e-21
 Match length 101
 % identity 54

NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
 >gi_100941_pir_S12140 zein Zc1 - maize
 >gi_100945_pir_B29017 zein 2 - maize
 >gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
 >gi_168666_ (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 298288
 Seq. ID LIB3151-001-P1-K1-D12
 Method BLASTN
 NCBI GI g168484
 BLAST score 279
 E value 1.0e-156
 Match length 355
 % identity 95

NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298289
 Seq. ID LIB3151-001-P1-K1-D7
 Method BLASTX
 NCBI GI g224513
 BLAST score 172
 E value 7.0e-13
 Match length 51
 % identity 75

NCBI Description zein M6 [Zea mays]

Seq. No. 298290
 Seq. ID LIB3151-001-P1-K1-D8
 Method BLASTX
 NCBI GI g135060
 BLAST score 405
 E value 1.0e-39
 Match length 90
 % identity 87

NCBI Description SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
 (SHRUNKEN-1) >gi_66570_pir_YUZMS sucrose synthase (EC
 2.4.1.13) - maize >gi_22486_emb_CAA26247_ (X02400) sucrose
 synthase [Zea mays] >gi_22488_emb_CAA26229_ (X02382)
 sucrose synthase [Zea mays]

Seq. No. 298291
 Seq. ID LIB3151-001-P1-K1-E12
 Method BLASTN
 NCBI GI g4185305

096311E-1001000

BLAST score	193
E value	1.0e-104
Match length	289
% identity	92
NCBI Description	Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete cds; and unknown genes
Seq. No.	298292
Seq. ID	LIB3151-001-P1-K1-E4
Method	BLASTX
NCBI GI	g1172977
BLAST score	217
E value	1.0e-17
Match length	92
% identity	50
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]
Seq. No.	298293
Seq. ID	LIB3151-001-P1-K1-E7
Method	BLASTX
NCBI GI	g2832243
BLAST score	180
E value	2.0e-13
Match length	74
% identity	55
NCBI Description	(AF031569) 22-kDa alpha zein 4 [Zea mays]
Seq. No.	298294
Seq. ID	LIB3151-001-P1-K1-F2
Method	BLASTN
NCBI GI	g22549
BLAST score	238
E value	1.0e-131
Match length	278
% identity	97
NCBI Description	Maize gene for a 27kDa storage protein, zein
Seq. No.	298295
Seq. ID	LIB3151-001-P1-K1-F4
Method	BLASTX
NCBI GI	g168695
BLAST score	157
E value	2.0e-10
Match length	89
% identity	46
NCBI Description	(M16218) gamma zein [Zea mays] >gi_225315_prf_1211356A zein gamma [Zea mays]
Seq. No.	298296
Seq. ID	LIB3151-001-P1-K1-F7
Method	BLASTN
NCBI GI	g168681
BLAST score	102
E value	4.0e-50

Match length 245
% identity 86
NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
>gi_270686_gb_I03333_Sequence 8 from Patent US

Seq. No. 298297
Seq. ID LIB3151-001-P1-K1-G10
Method BLASTN
NCBI GI g22549
BLAST score 33
E value 3.0e-09
Match length 61
% identity 89
NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 298298
Seq. ID LIB3151-001-P1-K1-G11
Method BLASTX
NCBI GI g22122
BLAST score 222
E value 2.0e-18
Match length 53
% identity 87
NCBI Description (X04050) alcohol dehydrogenase 1 [Zea mays] >gi_3420021
(AF050457) alcohol dehydrogenase 1 [Zea mays]

Seq. No. 298299
Seq. ID LIB3151-001-P1-K1-H11
Method BLASTN
NCBI GI g22549
BLAST score 113
E value 6.0e-57
Match length 197
% identity 89
NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 298300
Seq. ID LIB3151-001-P1-K1-H8
Method BLASTN
NCBI GI g168665
BLAST score 208
E value 1.0e-113
Match length 252
% identity 96
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 298301
Seq. ID LIB3151-002-P1-K1-A3
Method BLASTX
NCBI GI g121472
BLAST score 142
E value 7.0e-09
Match length 70
% identity 44
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -

maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298302
Seq. ID LIB3151-002-P1-K1-A7
Method BLASTX
NCBI GI g82660
BLAST score 162
E value 3.0e-11
Match length 62
% identity 56
NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment)
>gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

Seq. No. 298303
Seq. ID LIB3151-002-P1-K1-C2
Method BLASTX
NCBI GI g121472
BLAST score 149
E value 7.0e-22
Match length 106
% identity 54
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298304
Seq. ID LIB3151-002-P1-K1-C3
Method BLASTX
NCBI GI g135417
BLAST score 209
E value 7.0e-17
Match length 49
% identity 78
NCBI Description TUBULIN ALPHA-3 CHAIN >gi_100946_pir_JN0105 tubulin
alpha-3 chain - maize >gi_22150_emb_CAA44861_ (X63176)
Alpha-tubulin #3 [Zea mays] >gi_485377 (M60171) alpha-3
tubulin [Zea mays]

Seq. No. 298305
Seq. ID LIB3151-002-P1-K1-C5
Method BLASTX
NCBI GI g550542
BLAST score 183
E value 3.0e-26
Match length 133
% identity 51
NCBI Description (X81831) cytochrome P450 [Zea mays]
>gi_1850903_emb_CAA72196_ (Y11368) cytochrome p450 [Zea
mays]

Seq. No. 298306
Seq. ID LIB3151-002-P1-K1-C6

Method BLASTX
 NCBI GI g121472
 BLAST score 257
 E value 3.0e-22
 Match length 110
 % identity 45
 NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
 (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
 >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
 maize >gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor
 [Zea mays] >gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea
 mays] >gi_168485_(M16066) glutelin-2 [Zea mays]

Seq. No. 298307
 Seq. ID LIB3151-002-P1-K1-D1
 Method BLASTN
 NCBI GI g168679
 BLAST score 40
 E value 4.0e-13
 Match length 56
 % identity 93
 NCBI Description Maize 19 kDa zein mRNA, clone cZ19C2, complete cds.
 >gi_270687_gb_I03334_Sequence 9 from Patent US

Seq. No. 298308
 Seq. ID LIB3151-002-P1-K1-E2
 Method BLASTX
 NCBI GI g2832246
 BLAST score 367
 E value 4.0e-35
 Match length 124
 % identity 66
 NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]

Seq. No. 298309
 Seq. ID LIB3151-002-P1-K1-E3
 Method BLASTX
 NCBI GI g121472
 BLAST score 184
 E value 1.0e-13
 Match length 80
 % identity 49
 NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
 (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
 >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
 maize >gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor
 [Zea mays] >gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea
 mays] >gi_168485_(M16066) glutelin-2 [Zea mays]

Seq. No. 298310
 Seq. ID LIB3151-002-P1-K1-E5
 Method BLASTX
 NCBI GI g16073
 BLAST score 369
 E value 2.0e-35
 Match length 109
 % identity 70

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NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 298311
Seq. ID LIB3151-002-P1-K1-G1
Method BLASTN
NCBI GI g22215
BLAST score 70
E value 4.0e-31
Match length 312
% identity 84
NCBI Description Z.mays ZSF4C1 gene for zein

Seq. No. 298312
Seq. ID LIB3151-002-P1-K1-G5
Method BLASTX
NCBI GI g2146739
BLAST score 227
E value 1.0e-18
Match length 69
% identity 65
NCBI Description hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521 (U28214) hexokinase 1 [Arabidopsis thaliana]

Seq. No. 298313
Seq. ID LIB3151-002-P1-K1-G6
Method BLASTX
NCBI GI g168699
BLAST score 236
E value 7.0e-20
Match length 68
% identity 74
NCBI Description (M60836) zein [Zea mays]

Seq. No. 298314
Seq. ID LIB3151-002-P1-K1-H2
Method BLASTX
NCBI GI g168701
BLAST score 276
E value 1.0e-24
Match length 96
% identity 65
NCBI Description (M60837) zein [Zea mays]

Seq. No. 298315
Seq. ID LIB3151-002-P1-K1-H7
Method BLASTN
NCBI GI g168425
BLAST score 180
E value 9.0e-97
Match length 252
% identity 93
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds

Seq. No. 298316
Seq. ID LIB3151-003-Q1-K1-A10
Method BLASTX
NCBI GI g2832247

BLAST score 261
E value 9.0e-23
Match length 99
% identity 58
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]

Seq. No. 298317
Seq. ID LIB3151-003-Q1-K1-A11
Method BLASTN
NCBI GI g22514
BLAST score 33
E value 4.0e-09
Match length 168
% identity 80
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 298318
Seq. ID LIB3151-003-Q1-K1-A4
Method BLASTX
NCBI GI g141615
BLAST score 162
E value 2.0e-14
Match length 73
% identity 73
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
>gi_22536_emb_CAA24727_ (V01480) zein protein 3 [Zea mays]

Seq. No. 298319
Seq. ID LIB3151-003-Q1-K1-A5
Method BLASTX
NCBI GI g2440160
BLAST score 215
E value 1.0e-17
Match length 67
% identity 63
NCBI Description (Y14836) beta-galactosidase [Phagemid cloning vector pTZ19U]

Seq. No. 298320
Seq. ID LIB3151-003-Q1-K1-A9
Method BLASTX
NCBI GI g121472
BLAST score 205
E value 4.0e-16
Match length 98
% identity 45
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
mays] >gi_168485_(M16066) glutelin-2 [Zea mays]

Seq. No. 298321
Seq. ID LIB3151-003-Q1-K1-B12
Method BLASTX
NCBI GI g548852

BLAST score 353
E value 2.0e-33
Match length 82
% identity 78
NCBI Description 40S RIBOSOMAL PROTEIN S21 >gi_481227_pir_S38357 ribosomal protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S subunit ribosomal protein [Oryza sativa]

Seq. No. 298322
Seq. ID LIB3151-003-Q1-K1-C1
Method BLASTN
NCBI GI g168484
BLAST score 45
E value 2.0e-16
Match length 53
% identity 96
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298323
Seq. ID LIB3151-003-Q1-K1-C12
Method BLASTX
NCBI GI g4249662
BLAST score 168
E value 7.0e-12
Match length 87
% identity 45
NCBI Description (AF089810) Altered Response to Gravity [Arabidopsis thaliana]

Seq. No. 298324
Seq. ID LIB3151-003-Q1-K1-C4
Method BLASTX
NCBI GI g141597
BLAST score 214
E value 2.0e-17
Match length 108
% identity 44
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 298325
Seq. ID LIB3151-003-Q1-K1-C6
Method BLASTX
NCBI GI g168699
BLAST score 402
E value 3.0e-39
Match length 96
% identity 83
NCBI Description (M60836) zein [Zea mays]

Seq. No. 298326
Seq. ID LIB3151-003-Q1-K1-D1
Method BLASTX
NCBI GI g100925
BLAST score 219

E value 6.0e-18
Match length 84
% identity 49
NCBI Description zein, 27K - maize (fragment) >gi_22550_emb_CAA41175_ (X58197) 27kDa storage protein, zein [Zea mays]

Seq. No. 298327
Seq. ID LIB3151-003-Q1-K1-D10
Method BLASTX
NCBI GI g2982322
BLAST score 246
E value 2.0e-21
Match length 66
% identity 74
NCBI Description (AF051246) probable proteasome subunit [Picea mariana]

Seq. No. 298328
Seq. ID LIB3151-003-Q1-K1-D12
Method BLASTX
NCBI GI g133867
BLAST score 464
E value 2.0e-46
Match length 111
% identity 77
NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir_S16577 ribosomal protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays]

Seq. No. 298329
Seq. ID LIB3151-003-Q1-K1-E1
Method BLASTX
NCBI GI g224508
BLAST score 264
E value 5.0e-23
Match length 82
% identity 68
NCBI Description zein A20 [Zea mays]

Seq. No. 298330
Seq. ID LIB3151-003-Q1-K1-E10
Method BLASTX
NCBI GI g133867
BLAST score 494
E value 5.0e-50
Match length 114
% identity 83
NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir_S16577 ribosomal protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays]

Seq. No. 298331
Seq. ID LIB3151-003-Q1-K1-E11
Method BLASTX
NCBI GI g729737
BLAST score 195
E value 3.0e-15
Match length 83

% identity 55
NCBI Description HMG1/2-LIKE PROTEIN >gi_541981_pir_S39556 HMG protein -
fava bean

Seq. No. 298332
Seq. ID LIB3151-003-Q1-K1-E6
Method BLASTX
NCBI GI g141605
BLAST score 364
E value 6.0e-35
Match length 93
% identity 83
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) -
maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 298333
Seq. ID LIB3151-003-Q1-K1-F12
Method BLASTX
NCBI GI g4586031
BLAST score 280
E value 6.0e-25
Match length 64
% identity 83
NCBI Description (AC007109) unknown protein [Arabidopsis thaliana]

Seq. No. 298334
Seq. ID LIB3151-003-Q1-K1-F5
Method BLASTN
NCBI GI g168484
BLAST score 285
E value 1.0e-159
Match length 373
% identity 95
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298335
Seq. ID LIB3151-003-Q1-K1-G4
Method BLASTN
NCBI GI g22326
BLAST score 35
E value 3.0e-10
Match length 82
% identity 87
NCBI Description Z.mays gene for Hageman factor inhibitor

Seq. No. 298336
Seq. ID LIB3151-003-Q1-K1-G7
Method BLASTX
NCBI GI g168699
BLAST score 169
E value 3.0e-12
Match length 82
% identity 51
NCBI Description (M60836) zein [Zea mays]

Seq. No. 298337

Seq. ID LIB3151-003-Q1-K1-G9
Method BLASTX
NCBI GI g3757519
BLAST score 383
E value 6.0e-37
Match length 143
% identity 53
NCBI Description (AC005167) hypothetical protein [Arabidopsis thaliana]

Seq. No. 298338
Seq. ID LIB3151-003-Q1-K1-H11
Method BLASTX
NCBI GI g3292831
BLAST score 348
E value 4.0e-33
Match length 104
% identity 62
NCBI Description (AL031018) putative serine/threonine kinase [Arabidopsis thaliana]

Seq. No. 298339
Seq. ID LIB3151-003-Q1-K1-H5
Method BLASTN
NCBI GI g22528
BLAST score 125
E value 6.0e-64
Match length 347
% identity 85
NCBI Description Zea mays mRNA encoding a zein (clone A20)

Seq. No. 298340
Seq. ID LIB3151-004-Q1-K1-A11
Method BLASTN
NCBI GI g4140643
BLAST score 46
E value 8.0e-17
Match length 57
% identity 95
NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 298341
Seq. ID LIB3151-004-Q1-K1-A5
Method BLASTX
NCBI GI g100925
BLAST score 178
E value 4.0e-13
Match length 54
% identity 61
NCBI Description zein, 27K - maize (fragment) >gi_22550_emb_CAA41175_ (X58197) 27kDa storage protein, zein [Zea mays]

Seq. No. 298342
Seq. ID LIB3151-004-Q1-K1-B12
Method BLASTX
NCBI GI g121472
BLAST score 222

E value 4.0e-18
 Match length 97
 % identity 47
 NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
 (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
 >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
 maize >gi_22289_emb CAA26149 (X02230) glutelin-2 precursor
 [Zea mays] >gi_22517_emb CAA37594 (X53514) zein Zc2 [Zea
 mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

 Seq. No. 298343
 Seq. ID LIB3151-004-Q1-K1-C11
 Method BLASTX
 NCBI GI g141605
 BLAST score 445
 E value 2.0e-44
 Match length 100
 % identity 92
 NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
 >gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) -
 maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

 Seq. No. 298344
 Seq. ID LIB3151-004-Q1-K1-C5
 Method BLASTX
 NCBI GI g2340108
 BLAST score 327
 E value 2.0e-30
 Match length 109
 % identity 60
 NCBI Description (U65948) starch branching enzyme IIa [Zea mays]

 Seq. No. 298345
 Seq. ID LIB3151-004-Q1-K1-C8
 Method BLASTX
 NCBI GI g3157932
 BLAST score 161
 E value 2.0e-11
 Match length 78
 % identity 45
 NCBI Description (AC002131) Similar to hypothetical protein HYP1 gb_Z97338
 from A. thaliana. [Arabidopsis thaliana]

 Seq. No. 298346
 Seq. ID LIB3151-004-Q1-K1-D9
 Method BLASTX
 NCBI GI g141617
 BLAST score 259
 E value 2.0e-22
 Match length 64
 % identity 77
 NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
 >gi_100941_pir_S12140 zein Zc1 - maize
 >gi_100945_pir_B29017 zein 2 - maize
 >gi_22515_emb CAA37595 (X53515) zein Zc1 [Zea mays]
 >gi_168666 (M16460) 16-kDa zein protein [Zea mays]

09634016-401000

Seq. No. 298347
Seq. ID LIB3151-004-Q1-K1-E11
Method BLASTN
NCBI GI g22445
BLAST score 69
E value 2.0e-30
Match length 137
% identity 89
NCBI Description Zea mays ZMPMS1 gene for 19 kDa zein protein

Seq. No. 298348
Seq. ID LIB3151-004-Q1-K1-E12
Method BLASTN
NCBI GI g1037129
BLAST score 98
E value 1.0e-47
Match length 341
% identity 83
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298349
Seq. ID LIB3151-004-Q1-K1-E3
Method BLASTN
NCBI GI g535019
BLAST score 119
E value 3.0e-60
Match length 257
% identity 45
NCBI Description Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)

Seq. No. 298350
Seq. ID LIB3151-004-Q1-K1-E4
Method BLASTN
NCBI GI g22524
BLAST score 107
E value 4.0e-53
Match length 163
% identity 91
NCBI Description Zea mays mRNA encoding a zein (clone ZG31A)

Seq. No. 298351
Seq. ID LIB3151-004-Q1-K1-E6
Method BLASTN
NCBI GI g168484
BLAST score 84
E value 2.0e-39
Match length 128
% identity 91
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298352
Seq. ID LIB3151-004-Q1-K1-F10
Method BLASTX
NCBI GI g168691
BLAST score 271
E value 6.0e-24

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Match length 99
% identity 61
NCBI Description (M29628) zein [Zea mays]

Seq. No. 298353
Seq. ID LIB3151-004-Q1-K1-F11
Method BLASTX
NCBI GI g141598
BLAST score 170
E value 4.0e-12
Match length 44
% identity 75
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE ZG99)
>gi_72313_pir_ZIZM99_19K zein precursor (clone ZG99) - maize
>gi_22519_emb_CAA24717_ (V01470) zein [Zea mays]
>gi_22534_emb_CAA24726_ (V01479) zein [Zea mays]

Seq. No. 298354
Seq. ID LIB3151-004-Q1-K1-F3
Method BLASTN
NCBI GI g168484
BLAST score 161
E value 2.0e-85
Match length 348
% identity 87
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298355
Seq. ID LIB3151-004-Q1-K1-F9
Method BLASTX
NCBI GI g141603
BLAST score 550
E value 1.0e-56
Match length 135
% identity 87
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
>gi_72311_pir_ZIZM2_19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 298356
Seq. ID LIB3151-004-Q1-K1-G6
Method BLASTN
NCBI GI g4336204
BLAST score 38
E value 5.0e-12
Match length 46
% identity 96
NCBI Description Zea mays cytochrome b5 reductase (NFR) mRNA, complete cds

Seq. No. 298357
Seq. ID LIB3151-004-Q1-K1-H2
Method BLASTX
NCBI GI g1345838
BLAST score 236
E value 7.0e-20
Match length 58
% identity 76

NCBI Description PHYTOENE DEHYDROGENASE PRECURSOR (PHYTOENE DESATURASE)
 >gi_2130143_pir_S65060 phytoene desaturase precursor -
 maize >gi_1051180 (U37285) phytoene desaturase [Zea mays]

Seq. No. 298358
 Seq. ID LIB3151-004-Q1-K1-H6
 Method BLASTX
 NCBI GI g141600
 BLAST score 167
 E value 3.0e-16
 Match length 98
 % identity 54

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
 >gi_72315_pir_ZIZMB1 19K zein precursor (clone cZ19B1) -
 maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]

Seq. No. 298359
 Seq. ID LIB3151-004-Q1-K1-H9
 Method BLASTX
 NCBI GI g119748
 BLAST score 219
 E value 5.0e-18
 Match length 48
 % identity 83

NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC
 (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
 >gi_67241_pir_PASPY fructose-bisphosphatase (EC 3.1.3.11),
 cytosolic - spinach >gi_21245_emb_CAA43860_ (X61690)
 fructose-bisphosphatase [Spinacia oleracea]

Seq. No. 298360
 Seq. ID LIB3151-005-Q1-K1-A4
 Method BLASTN
 NCBI GI g168484
 BLAST score 280
 E value 1.0e-156
 Match length 328
 % identity 96

NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298361
 Seq. ID LIB3151-005-Q1-K1-B1
 Method BLASTX
 NCBI GI g419803
 BLAST score 218
 E value 1.0e-17
 Match length 83
 % identity 52

NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 298362
 Seq. ID LIB3151-005-Q1-K1-C7
 Method BLASTX
 NCBI GI g629861
 BLAST score 267
 E value 2.0e-23

Match length 125
% identity 51
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 298363
Seq. ID LIB3151-005-Q1-K1-E12
Method BLASTX
NCBI GI g266398
BLAST score 349
E value 4.0e-33
Match length 96
% identity 68
NCBI Description TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR INHIBITOR) (CHFI) >gi_68849_pir_TIZM1 trypsin/factor XIIa inhibitor precursor - maize >gi_22327_emb_CAA37998_ (X54064) corn Hageman factor inhibitor [Zea mays]

Seq. No. 298364
Seq. ID LIB3151-005-Q1-K1-E5
Method BLASTX
NCBI GI g141608
BLAST score 316
E value 3.0e-29
Match length 118
% identity 60
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655 zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa zein [Zea mays]

Seq. No. 298365
Seq. ID LIB3151-005-Q1-K1-E8
Method BLASTX
NCBI GI g168701
BLAST score 169
E value 5.0e-12
Match length 53
% identity 58
NCBI Description (M60837) zein [Zea mays]

Seq. No. 298366
Seq. ID LIB3151-005-Q1-K1-E9
Method BLASTX
NCBI GI g719291
BLAST score 197
E value 2.0e-15
Match length 83
% identity 46
NCBI Description (U19134) unknown [Arabidopsis thaliana]
>gi_1095007_prf_2107236A SABRE gene [Arabidopsis thaliana]

Seq. No. 298367
Seq. ID LIB3151-005-Q1-K1-F1
Method BLASTN
NCBI GI g1037129
BLAST score 349
E value 0.0e+00

Match length 445
% identity 95
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298368
Seq. ID LIB3151-005-Q1-K1-F10
Method BLASTX
NCBI GI g168699
BLAST score 337
E value 1.0e-31
Match length 108
% identity 67
NCBI Description (M60836) zein [Zea mays]

Seq. No. 298369
Seq. ID LIB3151-005-Q1-K1-F7
Method BLASTX
NCBI GI g121472
BLAST score 228
E value 5.0e-19
Match length 88
% identity 49
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb_CAA26149 (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594 (X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298370
Seq. ID LIB3151-005-Q1-K1-G11
Method BLASTN
NCBI GI g168665
BLAST score 46
E value 5.0e-17
Match length 217
% identity 81
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 298371
Seq. ID LIB3151-005-Q1-K1-G4
Method BLASTX
NCBI GI g584706
BLAST score 384
E value 2.0e-37
Match length 97
% identity 77
NCBI Description ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)
>gi_2130066_pir_JC5124 aspartate transaminase (EC
2.6.1.1), cytoplasmic - rice >gi_287298_dbj_BAA03504-
(D14673) aspartate aminotransferase [Oryza sativa]

Seq. No. 298372
Seq. ID LIB3151-005-Q1-K1-G5
Method BLASTX
NCBI GI g72307

BLAST score 351
E value 2.0e-33
Match length 112
% identity 67
NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686
(J01246) 26.99 kd zein protein [Zea mays]

Seq. No. 298373
Seq. ID LIB3151-005-Q1-K1-H11
Method BLASTX
NCBI GI g141597
BLAST score 221
E value 1.0e-32
Match length 130
% identity 62
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 298374
Seq. ID LIB3151-006-Q1-K1-B2
Method BLASTX
NCBI GI g141610
BLAST score 184
E value 1.0e-13
Match length 51
% identity 75
NCBI Description ZEIN-ALPHA PRECURSOR (CLONE Z4)

Seq. No. 298375
Seq. ID LIB3151-006-Q1-K1-C3
Method BLASTX
NCBI GI g168664
BLAST score 282
E value 2.0e-25
Match length 94
% identity 60
NCBI Description (M13507) zein protein precursor [Zea mays]

Seq. No. 298376
Seq. ID LIB3151-006-Q1-K1-C6
Method BLASTX
NCBI GI g141617
BLAST score 271
E value 8.0e-24
Match length 66
% identity 77
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
>gi_168666_ (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 298377
Seq. ID LIB3151-006-Q1-K1-C9
Method BLASTX

09634016 4104000

NCBI GI	g2623248
BLAST score	471
E value	3.0e-47
Match length	145
% identity	67
NCBI Description	(AF030882) SU1 isoamylase [Zea mays]
Seq. No.	298378
Seq. ID	LIB3151-006-Q1-K1-D11
Method	BLASTX
NCBI GI	g4185308
BLAST score	175
E value	9.0e-13
Match length	93
% identity	46
NCBI Description	(AF090446) 22-kDa alpha zein protein 21 [Zea mays]
Seq. No.	298379
Seq. ID	LIB3151-006-Q1-K1-D5
Method	BLASTX
NCBI GI	g629861
BLAST score	233
E value	2.0e-19
Match length	110
% identity	50
NCBI Description	zein Zd1, 19K - maize >gi_535020_ emb_CAA47639_ (X67203) zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.	298380
Seq. ID	LIB3151-006-Q1-K1-E8
Method	BLASTN
NCBI GI	g168425
BLAST score	40
E value	2.0e-13
Match length	192
% identity	81
NCBI Description	Zea mays brittle-1 protein (bt1) mRNA, complete cds
Seq. No.	298381
Seq. ID	LIB3151-006-Q1-K1-F1
Method	BLASTN
NCBI GI	g22514
BLAST score	156
E value	2.0e-82
Match length	312
% identity	88
NCBI Description	Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
Seq. No.	298382
Seq. ID	LIB3151-006-Q1-K1-F4
Method	BLASTX
NCBI GI	g2345154
BLAST score	279
E value	6.0e-31
Match length	94
% identity	81
NCBI Description	(AF015522) ribosomal protein S4 [Zea mays]

Seq. No. 298383
Seq. ID LIB3151-006-Q1-K1-G9
Method BLASTX
NCBI GI g168701
BLAST score 197
E value 2.0e-15
Match length 73
% identity 60
NCBI Description (M60837) zein [Zea mays] *

Seq. No. 298384
Seq. ID LIB3151-006-Q1-K1-H12
Method BLASTX
NCBI GI g22220
BLAST score 165
E value 2.0e-11
Match length 76
% identity 49
NCBI Description (X55723) 22 kD zein [Zea mays]

Seq. No. 298385
Seq. ID LIB3151-006-Q1-K1-H2
Method BLASTX
NCBI GI g141608
BLAST score 294
E value 2.0e-30
Match length 113
% identity 68
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]

Seq. No. 298386
Seq. ID LIB3151-006-Q1-K1-H8
Method BLASTX
NCBI GI g141615
BLAST score 273
E value 2.0e-25
Match length 89
% identity 78
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
>gi_22536_emb_CAA24727_ (V01480) zein protein 3 [Zea mays]

Seq. No. 298387
Seq. ID LIB3151-007-Q1-K1-A12
Method BLASTN
NCBI GI g1037129
BLAST score 314
E value 1.0e-176
Match length 376
% identity 96
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298388
Seq. ID LIB3151-007-Q1-K1-A2

Method	BLASTX
NCBI GI	g168699
BLAST score	566
E value	2.0e-58
Match length	142
% identity	57
NCBI Description	(M60836) zein [Zea mays]
Seq. No.	298389
Seq. ID	LIB3151-007-Q1-K1-A3
Method	BLASTX
NCBI GI	g121472
BLAST score	384
E value	5.0e-37
Match length	142
% identity	54
NCBI Description	GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2) >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) - maize >gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea mays] >gi_168485_(M16066) glutelin-2 [Zea mays]
Seq. No.	298390
Seq. ID	LIB3151-007-Q1-K1-A4
Method	BLASTX
NCBI GI	g141599
BLAST score	367
E value	4.0e-35
Match length	101
% identity	75
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19A2) >gi_72316_pir_ZIZMA2 19K zein precursor (clone cz19A2) - maize (fragment) >gi_168670_(M12142) 19 kDa zein protein [Zea mays]
Seq. No.	298391
Seq. ID	LIB3151-007-Q1-K1-B9
Method	BLASTX
NCBI GI	g141603
BLAST score	420
E value	2.0e-41
Match length	104
% identity	87
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20) >gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize >gi_22529_emb_CAA24723_(V01476) zein [Zea mays]
Seq. No.	298392
Seq. ID	LIB3151-007-Q1-K1-C10
Method	BLASTX
NCBI GI	g3549665
BLAST score	140
E value	9.0e-09
Match length	74
% identity	50
NCBI Description	(AL031394) hypothetical protein [Arabidopsis thaliana]

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Seq. No. 298393
Seq. ID LIB3151-007-Q1-K1-C11
Method BLASTX
NCBI GI g141605
BLAST score 177
E value 4.0e-13
Match length 71
% identity 54
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) - maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 298394
Seq. ID LIB3151-007-Q1-K1-C12
Method BLASTN
NCBI GI g22516
BLAST score 160
E value 8.0e-85
Match length 312
% identity 88
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298395
Seq. ID LIB3151-007-Q1-K1-C2
Method BLASTX
NCBI GI g141597
BLAST score 230
E value 2.0e-27
Match length 119
% identity 60
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2] [Zea mays]

Seq. No. 298396
Seq. ID LIB3151-007-Q1-K1-C5
Method BLASTX
NCBI GI g419803
BLAST score 162
E value 6.0e-16
Match length 109
% identity 46
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 298397
Seq. ID LIB3151-007-Q1-K1-D11
Method BLASTN
NCBI GI g22514
BLAST score 69
E value 6.0e-31
Match length 125
% identity 89
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

09630114000

Seq. No. 298398
Seq. ID LIB3151-007-Q1-K1-D3
Method BLASTX
NCBI GI g141616
BLAST score 290
E value 4.0e-26
Match length 118
% identity 52
NCBI Description ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
>gi_168662 (M12147) 15 kDa zein protein [Zea mays]

Seq. No. 298399
Seq. ID LIB3151-007-Q1-K1-E5
Method BLASTX
NCBI GI g141605
BLAST score 186
E value 3.0e-14
Match length 62
% identity 68
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) - maize
>gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 298400
Seq. ID LIB3151-007-Q1-K1-E6
Method BLASTX
NCBI GI g2832243
BLAST score 358
E value 5.0e-34
Match length 126
% identity 61
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298401
Seq. ID LIB3151-007-Q1-K1-F9
Method BLASTN
NCBI GI g22516
BLAST score 133
E value 1.0e-68
Match length 241
% identity 89
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298402
Seq. ID LIB3151-007-Q1-K1-G10
Method BLASTX
NCBI GI g141617
BLAST score 353
E value 2.0e-33
Match length 82
% identity 80
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595 (X53515) zein Zc1 [Zea mays]
>gi_168666 (M16460) 16-kDa zein protein [Zea mays]

DRAFT

Seq. No.	298403
Seq. ID	LIB3151-007-Q1-K1-G11
Method	BLASTN
NCBI GI	g168673
BLAST score	46
E value	7.0e-17
Match length	66
% identity	92
NCBI Description	Maize 19 kDa zein mRNA, clone cZ19B1, complete cds
Seq. No.	298404
Seq. ID	LIB3151-007-Q1-K1-G7
Method	BLASTX
NCBI GI	g141597
BLAST score	313
E value	1.0e-28
Match length	140
% identity	57
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30) >gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2] [Zea mays]
Seq. No.	298405
Seq. ID	LIB3151-007-Q1-K1-H3
Method	BLASTX
NCBI GI	g141597
BLAST score	286
E value	9.0e-26
Match length	102
% identity	66
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30) >gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2] [Zea mays]
Seq. No.	298406
Seq. ID	LIB3151-008-Q1-K1-A11
Method	BLASTX
NCBI GI	g82660
BLAST score	156
E value	8.0e-11
Match length	64
% identity	55
NCBI Description	19K zein precursor (clone ZG31A) - maize (fragment) >gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]
Seq. No.	298407
Seq. ID	LIB3151-008-Q1-K1-A12
Method	BLASTX
NCBI GI	g168701
BLAST score	407
E value	9.0e-40
Match length	120
% identity	73
NCBI Description	(M60837) zein [Zea mays]

09634016-101000

Seq. No. 298408
Seq. ID LIB3151-008-Q1-K1-A3
Method BLASTX
NCBI GI g82660
BLAST score 331
E value 6.0e-31
Match length 94
% identity 72
NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment)
>gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

Seq. No. 298409
Seq. ID LIB3151-008-Q1-K1-C10
Method BLASTX
NCBI GI g168701
BLAST score 288
E value 7.0e-26
Match length 89
% identity 62
NCBI Description (M60837) zein [Zea mays]

Seq. No. 298410
Seq. ID LIB3151-008-Q1-K1-D10
Method BLASTX
NCBI GI g141616
BLAST score 210
E value 6.0e-17
Match length 85
% identity 52
NCBI Description ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
>gi_168662 (M12147) 15 kDa zein protein [Zea mays]

Seq. No. 298411
Seq. ID LIB3151-008-Q1-K1-F10
Method BLASTX
NCBI GI g508545
BLAST score 359
E value 3.0e-34
Match length 123
% identity 64
NCBI Description (L34340) zein [Zea mays]

Seq. No. 298412
Seq. ID LIB3151-008-Q1-K1-F11
Method BLASTX
NCBI GI g629861
BLAST score 394
E value 3.0e-38
Match length 138
% identity 61
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 298413
Seq. ID LIB3151-008-Q1-K1-F12
Method BLASTN
NCBI GI g22514

BLAST score 90
E value 3.0e-43
Match length 226
% identity 85
NCBI Description Maize Zcl gene for Zein Zcl (14 kD zein-2)

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Seq. No.          298414
Seq. ID          LIB3151-008-Q1-K1-G12
Method          BLASTX
NCBI GI          g141617
BLAST score      293
E value          2.0e-26
Match length     98
% identity        57
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
                  >gi_100941_pir_S12140 zein Zc1 - maize
                  >gi_100945_pir_B29017 zein 2 - maize
                  >gi_22515_emb_CAA37595_(X53515) zein Zc1 [Zea mays]
                  >gi_168666_(M16460) 16-kDa zein protein [Zea mays]

```

Seq. No. 298415
Seq. ID LIB3151-009-Q1-K1-A8
Method BLASTX
NCBI GI g141605
BLAST score 201
E value 8.0e-16
Match length 84
% identity 55
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) -
maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 298416
Seq. ID LIB3151-009-Q1-K1-C10
Method BLASTN
NCBI GI g168665
BLAST score 41
E value 4.0e-14
Match length 153
% identity 82
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 298417
Seq. ID LIB3151-009-Q1-K1-C6
Method BLASTX
NCBI GI g168695
BLAST score 249
E value 1.0e-21
Match length 79
% identity 62
NCBI Description (M16218) gamma zein [Zea mays] >gi_225315_prf_1211356A
zein gamma [Zea mays]

Seq. No. 298418
Seq. ID LIB3151-009-Q1-K1-C8
Method BLASTN
NCBI GI q168704

BLAST score 34
E value 1.0e-09
Match length 42
% identity 95
NCBI Description Zea mays zein protein gene, complete cds

Seq. No. 298419
Seq. ID LIB3151-009-Q1-K1-C9
Method BLASTN
NCBI GI g22544
BLAST score 124
E value 3.0e-63
Match length 144
% identity 97
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)

Seq. No. 298420
Seq. ID LIB3151-009-Q1-K1-D2
Method BLASTN
NCBI GI g508544
BLAST score 118
E value 9.0e-60
Match length 238
% identity 88
NCBI Description Zea mays 24-kD alpha-zein gene (floury2), complete cds

Seq. No. 298421
Seq. ID LIB3151-009-Q1-K1-D8
Method BLASTX
NCBI GI g2832243
BLAST score 336
E value 1.0e-31
Match length 100
% identity 72
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298422
Seq. ID LIB3151-009-Q1-K1-E2
Method BLASTX
NCBI GI g3122673
BLAST score 236
E value 4.0e-20
Match length 62
% identity 74
NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_ (Z97341) ribosomal protein [Arabidopsis thaliana]

Seq. No. 298423
Seq. ID LIB3151-009-Q1-K1-E6
Method BLASTN
NCBI GI g168704
BLAST score 45
E value 2.0e-16
Match length 117
% identity 85
NCBI Description Zea mays zein protein gene, complete cds

Seq. No. 298424
Seq. ID LIB3151-009-Q1-K1-G10
Method BLASTX
NCBI GI g141612
BLAST score 251
E value 5.0e-30
Match length 108
% identity 36
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE 22C2)
>gi_72306_pir_ZIZMC2 22K zein precursor (clone cZ22C2) -
maize (fragment) >gi_168688 (M12141) 22 kDa zein protein
[Zea mays]

Seq. No. 298425
Seq. ID LIB3151-009-Q1-K1-G6
Method BLASTN
NCBI GI g1037129
BLAST score 241
E value 1.0e-133
Match length 325
% identity 94
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298426
Seq. ID LIB3151-009-Q1-K1-H2
Method BLASTX
NCBI GI g224508
BLAST score 386
E value 6.0e-39
Match length 119
% identity 75
NCBI Description zein A20 [Zea mays]

Seq. No. 298427
Seq. ID LIB3151-009-Q1-K1-H9
Method BLASTN
NCBI GI g22516
BLAST score 50
E value 2.0e-19
Match length 82
% identity 90
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298428
Seq. ID LIB3151-010-Q1-K1-B10
Method BLASTX
NCBI GI g419803
BLAST score 380
E value 1.0e-36
Match length 112
% identity 66
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea
mays]

Seq. No. 298429
Seq. ID LIB3151-010-Q1-K1-B5

Method BLASTN
NCBI GI g168685
BLAST score 60
E value 3.0e-25
Match length 248
% identity 82
NCBI Description Maize 22 kd (Mw=26.99 kd) zein protein 3, mRNA

Seq. No. 298430
Seq. ID LIB3151-010-Q1-K1-C8
Method BLASTN
NCBI GI g22288
BLAST score 54
E value 1.0e-21
Match length 174
% identity 83
NCBI Description Maize mRNA fragment for endosperm glutelin-2

Seq. No. 298431
Seq. ID LIB3151-010-Q1-K1-D10
Method BLASTX
NCBI GI g168697
BLAST score 301
E value 2.0e-27
Match length 86
% identity 77
NCBI Description (M60835) zein [Zea mays]

Seq. No. 298432
Seq. ID LIB3151-010-Q1-K1-D6
Method BLASTX
NCBI GI g168695
BLAST score 224
E value 2.0e-18
Match length 106
% identity 50
NCBI Description (M16218) gamma zein [Zea mays] >gi_225315_prf_1211356A
zein gamma [Zea mays]

Seq. No. 298433
Seq. ID LIB3151-010-Q1-K1-D7
Method BLASTN
NCBI GI g22445
BLAST score 38
E value 4.0e-12
Match length 98
% identity 85
NCBI Description Zea mays ZMPMS1 gene for 19 kDa zein protein

Seq. No. 298434
Seq. ID LIB3151-010-Q1-K1-E9
Method BLASTN
NCBI GI g22172
BLAST score 72
E value 2.0e-32
Match length 124
% identity 90

NCBI Description Maize ATP2 mRNA for mitochondrial ATP synthase beta subunit

Seq. No. 298435
Seq. ID LIB3151-010-Q1-K1-F2
Method BLASTN
NCBI GI g168665
BLAST score 208
E value 1.0e-113
Match length 236
% identity 97

NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 298436
Seq. ID LIB3151-010-Q1-K1-F9
Method BLASTX
NCBI GI g419803
BLAST score 285
E value 1.0e-25
Match length 110
% identity 53

NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 298437
Seq. ID LIB3151-010-Q1-K1-G1
Method BLASTX
NCBI GI g100938
BLAST score 200
E value 8.0e-16
Match length 84
% identity 56

NCBI Description zein precursor - maize >gi_22442_emb_CAA32513_ (X14335)
zein precursor (AA -21 to 90) [Zea mays]

Seq. No. 298438
Seq. ID LIB3151-010-Q1-K1-G10
Method BLASTX
NCBI GI g16073
BLAST score 182
E value 2.0e-13
Match length 101
% identity 46

NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 298439
Seq. ID LIB3151-010-Q1-K1-H7
Method BLASTN
NCBI GI g22516
BLAST score 287
E value 1.0e-160
Match length 329
% identity 97

NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298440
Seq. ID LIB3151-011-Q1-K1-A11
Method BLASTN

NCBI GI g168665
BLAST score 163
E value 1.0e-86
Match length 230
% identity 94
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 298441
Seq. ID LIB3151-011-Q1-K1-B12
Method BLASTX
NCBI GI g121472
BLAST score 158
E value 3.0e-11
Match length 41
% identity 73
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb_CAA26149 (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594 (X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298442
Seq. ID LIB3151-011-Q1-K1-B4
Method BLASTX
NCBI GI g224508
BLAST score 270
E value 6.0e-24
Match length 79
% identity 78
NCBI Description zein A20 [Zea mays]

Seq. No. 298443
Seq. ID LIB3151-011-Q1-K1-C1
Method BLASTX
NCBI GI g168691
BLAST score 189
E value 1.0e-14
Match length 73
% identity 55
NCBI Description (M29628) zein [Zea mays]

Seq. No. 298444
Seq. ID LIB3151-011-Q1-K1-C7
Method BLASTX
NCBI GI g419803
BLAST score 264
E value 3.0e-23
Match length 92
% identity 59
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea
mays]

Seq. No. 298445
Seq. ID LIB3151-011-Q1-K1-C8
Method BLASTN
NCBI GI g1037129

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BLAST score 234
E value 1.0e-129
Match length 362
% identity 91
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298446
Seq. ID LIB3151-011-Q1-K1-E11
Method BLASTN
NCBI GI g22549
BLAST score 52
E value 1.0e-20
Match length 148
% identity 84
NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 298447
Seq. ID LIB3151-011-Q1-K1-E6
Method BLASTN
NCBI GI g22544
BLAST score 109
E value 2.0e-54
Match length 133
% identity 96
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)

Seq. No. 298448
Seq. ID LIB3151-011-Q1-K1-F12
Method BLASTX
NCBI GI g629861
BLAST score 236
E value 9.0e-28
Match length 98
% identity 66
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 298449
Seq. ID LIB3151-011-Q1-K1-F3
Method BLASTX
NCBI GI g2832243
BLAST score 141
E value 2.0e-15
Match length 102
% identity 56
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298450
Seq. ID LIB3151-011-Q1-K1-G9
Method BLASTX
NCBI GI g168701
BLAST score 548
E value 3.0e-56
Match length 138
% identity 82
NCBI Description (M60837) zein [Zea mays]

Seq. No. 298451
Seq. ID LIB3151-011-Q1-K1-H11
Method BLASTN
NCBI GI g168698
BLAST score 46
E value 7.0e-17
Match length 157
% identity 83
NCBI Description Z.mays zein mRNA, complete cds

Seq. No. 298452
Seq. ID LIB3151-012-Q1-K1-A11
Method BLASTN
NCBI GI g535019
BLAST score 64
E value 2.0e-27
Match length 136
% identity 44
NCBI Description Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)

Seq. No. 298453
Seq. ID LIB3151-012-Q1-K1-A3
Method BLASTX
NCBI GI g141610
BLAST score 172
E value 3.0e-12
Match length 64
% identity 56
NCBI Description ZEIN-ALPHA PRECURSOR (CLONE Z4)

Seq. No. 298454
Seq. ID LIB3151-012-Q1-K1-A8
Method BLASTX
NCBI GI g419803
BLAST score 247
E value 3.0e-21
Match length 84
% identity 58
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 298455
Seq. ID LIB3151-012-Q1-K1-B7
Method BLASTX
NCBI GI g82660
BLAST score 450
E value 9.0e-45
Match length 147
% identity 65
NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment)
>gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

Seq. No. 298456
Seq. ID LIB3151-012-Q1-K1-C10
Method BLASTN
NCBI GI g168704

BLAST score 68
E value 3.0e-30
Match length 87
% identity 94
NCBI Description Zea mays zein protein gene, complete cds

Seq. No. 298457
Seq. ID LIB3151-012-Q1-K1-C12
Method BLASTX
NCBI GI g141604
BLAST score 415
E value 1.0e-40
Match length 132
% identity 71
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C1)
>gi_72310_pir_ZIZM91 19K zein precursor (clone cZ19C1) -
maize >gi_168678 (M12146) 19 kDa zein protein [Zea mays]

Seq. No. 298458
Seq. ID LIB3151-012-Q1-K1-C6
Method BLASTX
NCBI GI g224507
BLAST score 173
E value 1.0e-19
Match length 93
% identity 61
NCBI Description zein A1 [Zea mays]

Seq. No. 298459
Seq. ID LIB3151-012-Q1-K1-D12
Method BLASTN
NCBI GI g168677
BLAST score 34
E value 6.0e-10
Match length 50
% identity 94
NCBI Description Maize 19 kDa zein mRNA, clone cZ19C1, complete cds

Seq. No. 298460
Seq. ID LIB3151-012-Q1-K1-D3
Method BLASTX
NCBI GI g141617
BLAST score 229
E value 5.0e-19
Match length 100
% identity 51
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595 (X53515) zein Zc1 [Zea mays]
>gi_168666 (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 298461
Seq. ID LIB3151-012-Q1-K1-D6
Method BLASTN
NCBI GI g168484
BLAST score 192

E value 1.0e-104
Match length 386
% identity 94
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298462
Seq. ID LIB3151-012-Q1-K1-E12
Method BLASTX
NCBI GI g224507
BLAST score 178
E value 4.0e-13
Match length 63
% identity 60
NCBI Description zein A1 [Zea mays]

Seq. No. 298463
Seq. ID LIB3151-012-Q1-K1-E3
Method BLASTX
NCBI GI g100940
BLAST score 265
E value 3.0e-23
Match length 91
% identity 60
NCBI Description zein zA1 - maize

Seq. No. 298464
Seq. ID LIB3151-012-Q1-K1-E6
Method BLASTN
NCBI GI g168675
BLAST score 70
E value 2.0e-31
Match length 114
% identity 91
NCBI Description Maize mutant zein (zE19) gene, complete cds

Seq. No. 298465
Seq. ID LIB3151-012-Q1-K1-F11
Method BLASTN
NCBI GI g22516
BLAST score 363
E value 0.0e+00
Match length 423
% identity 96
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298466
Seq. ID LIB3151-012-Q1-K1-F5
Method BLASTN
NCBI GI g168692
BLAST score 62
E value 2.0e-26
Match length 216
% identity 88
NCBI Description Maize zein mRNA, complete cds, clone ZG7

Seq. No. 298467
Seq. ID LIB3151-012-Q1-K1-G5

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Method BLASTX
 NCBI GI g1332579
 BLAST score 642
 E value 2.0e-67
 Match length 151
 % identity 9
 NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

 Seq. No. 298468
 Seq. ID LIB3151-012-Q1-K1-G7
 Method BLASTX
 NCBI GI g168695
 BLAST score 143
 E value 9.0e-09
 Match length 28
 % identity 93
 NCBI Description (M16218) gamma zein [Zea mays] >gi_225315_prf_1211356A
 zein gamma [Zea mays]

 Seq. No. 298469
 Seq. ID LIB3151-012-Q1-K1-H11
 Method BLASTX
 NCBI GI g121472
 BLAST score 254
 E value 9.0e-23
 Match length 118
 % identity 50
 NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
 (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
 >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
 maize >gi_22289_emb_CAA26149 (X02230) glutelin-2 precursor
 [Zea mays] >gi_22517_emb_CAA37594 (X53514) zein Zc2 [Zea
 mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

 Seq. No. 298470
 Seq. ID LIB3151-012-Q1-K1-H7
 Method BLASTN
 NCBI GI g22514
 BLAST score 89
 E value 2.0e-42
 Match length 222
 % identity 90
 NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

 Seq. No. 298471
 Seq. ID LIB3151-012-Q1-K1-H8
 Method BLASTX
 NCBI GI g82660
 BLAST score 203
 E value 5.0e-16
 Match length 59
 % identity 69
 NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment)
 >gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

 Seq. No. 298472
 Seq. ID LIB3151-013-Q1-K1-B11

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Method BLASTX
NCBI GI g951449
BLAST score 498
E value 2.0e-50
Match length 149
% identity 65
NCBI Description (L46681) aspartic protease precursor [Lycopersicon esculentum]

Seq. No. 298473
Seq. ID LIB3151-013-Q1-K1-B3
Method BLASTX
NCBI GI g2995405
BLAST score 281
E value 6.0e-25
Match length 86
% identity 59
NCBI Description (Y12432) polyprotein [Ananas comosus]

Seq. No. 298474
Seq. ID LIB3151-013-Q1-K1-B5
Method BLASTX
NCBI GI g3094012
BLAST score 204
E value 5.0e-16
Match length 79
% identity 59
NCBI Description (AF060569) cold-regulated LTCOR12 [Lavatera thuringiaca]

Seq. No. 298475
Seq. ID LIB3151-013-Q1-K1-B9
Method BLASTX
NCBI GI g3885334
BLAST score 153
E value 6.0e-10
Match length 73
% identity 51
NCBI Description (AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No. 298476
Seq. ID LIB3151-013-Q1-K1-C2
Method BLASTX
NCBI GI g3540180
BLAST score 171
E value 4.0e-12
Match length 84
% identity 50
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No. 298477
Seq. ID LIB3151-013-Q1-K1-C8
Method BLASTX
NCBI GI g100484
BLAST score 512
E value 5.0e-52
Match length 147